



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(21) International Application Number: <b>PCT/US97/17618</b> (22) International Filing Date: <b>1 October 1997 (01.10.97)</b> (30) Priority Data: <table border="0"> <tr><td>08/724,643</td><td>1 October 1996 (01.10.96)</td><td>US</td></tr> <tr><td>08/844,419</td><td>18 April 1997 (18.04.97)</td><td>US</td></tr> <tr><td>08/846,017</td><td>25 April 1997 (25.04.97)</td><td>US</td></tr> <tr><td>08/851,843</td><td>6 May 1997 (06.05.97)</td><td>US</td></tr> <tr><td>08/854,050</td><td>9 May 1997 (09.05.97)</td><td>US</td></tr> <tr><td>08/915,503</td><td>14 August 1997 (14.08.97)</td><td>US</td></tr> <tr><td>08/911,312</td><td>14 August 1997 (14.08.97)</td><td>US</td></tr> <tr><td>08/912,951</td><td>14 August 1997 (14.08.97)</td><td>US</td></tr> </table> (71) Applicants (for all designated States except US): GERON CORPORATION [US/US]; 230 Constitution Drive, Menlo Park, CA 94025 (US). UNIVERSITY TECHNOLOGY CORPORATION [US/US]; Suite 250, 3101 Iris Avenue, Boulder, CO 80301 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): CECH, Thomas, R. [US/US]; 1545 Rockmont Circle, Boulder, CO 80303 (US). LINGNER, Joachim [CH/US]; 360-30th Street, Boulder, CO 80303 (US). NAKAMURA, Toru [JP/US]; 4940 Thun-		08/724,643	1 October 1996 (01.10.96)	US	08/844,419	18 April 1997 (18.04.97)	US	08/846,017	25 April 1997 (25.04.97)	US	08/851,843	6 May 1997 (06.05.97)	US	08/854,050	9 May 1997 (09.05.97)	US	08/915,503	14 August 1997 (14.08.97)	US	08/911,312	14 August 1997 (14.08.97)	US	08/912,951	14 August 1997 (14.08.97)	US	derbird Circle #204, Boulder, CO 80303 (US). CHAPMAN, Karen, B. [US/US]; 71 Cloud View Road, Sausalito, CA 94965 (US). MORIN, Gregg, B. [US/US]; 3407 Janice Way, Palo Alto, CA 94303 (US). HARLEY, Calvin, B. [CA/US]; 1730 University Avenue, Palo Alto, CA 94301 (US). ANDREWS, William, H. [US/US]; 6102 Park Avenue, Richmond, CA 94805 (US). (74) Agents: SMITH, William, M. et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> Without international search report and to be republished upon receipt of that report.	
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(54) Title: <b>TELOMERASE REVERSE TRANSCRIPTASE</b>																											
(57) Abstract  The present invention is directed to novel telomerase nucleic acids and amino acids. In particular, the present invention is directed to nucleic acid and amino acid sequences encoding various telomerase protein subunits and motifs, including the 123 kDa and 43 kDa telomerase protein subunits of <i>Euplotes aediculatus</i> , and related sequences from <i>Schizosaccharomyces</i> , <i>Saccharomyces</i> sequences, and human telomerase. The present invention is also directed to polypeptides comprising these telomerase protein subunits, as well as functional polypeptides and ribonucleoproteins that contain these subunits.																											

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## TELOMERASE REVERSE TRANSCRIPTASE

### FIELD OF THE INVENTION

5 The present invention provides novel telomerase genes and proteins and relates to the cloning and characterization of the catalytic protein component of telomerase, referred to as telomerase reverse transcriptase ("TRT").

10 In particular, the present invention is directed to a telomerase isolated from *Euplotes aediculatus*, the two polypeptide subunits of this telomerase of 123 and 43 kDa, as well as polypeptides, nucleic acids and sequences of the *Schizosaccharomyces*, other yeast, *Tetrahymena*, other fungi, mouse and other mammalian homologs of the *E. aediculatus* telomerase.

### BACKGROUND OF THE INVENTION

15 Telomeres, the protein-DNA structures physically located on the ends of the eukaryotic organisms, are required for chromosome stability and are involved in chromosomal organization within the nucleus (*See e.g.*, Zakian, Science 270:1601 [1995]; Blackburn and Gall, J. Mol. Biol., 120:33 [1978]; Oka *et al.*, Gene 10:301 [1980]; and Klobutcher *et al.*, Proc. Natl. Acad. Sci., 78:3015 [1981]). Telomeres are believed to be essential in such organisms as yeasts and probably most other  
20 eukaryotes, as they allow cells to distinguish intact from broken chromosomes, protect chromosomes from degradation, and act as substrates for novel replication mechanisms. Telomeres are generally replicated in a complex, cell cycle, and developmentally regulated manner by "telomerase," a telomere-specific DNA polymerase. However, telomerase-independent means for telomere maintenance have been described. In  
25 recent years, much attention has been focused on telomeres, as telomere loss has been associated with chromosomal changes such as those that occur in cancer and aging.

#### Telomeric DNA

In most organisms, telomeric DNA has been reported to consist of a tandem array of very simple sequences, which in many cases are short and precise. Typically,

telomeres consist of simple repetitive sequences rich in G residues in the strand that runs 5' to 3' toward the chromosomal end. For example, telomeric DNA in *Tetrahymena* is comprised of sequence T<sub>2</sub>G<sub>4</sub>, while in *Oxytricha*, the sequence is T<sub>4</sub>G<sub>4</sub>, and in humans the sequence is T<sub>2</sub>AG<sub>3</sub> (See e.g., Zakian, Science 270:1601 [1995]; and Lingner *et al.*, Genes Develop., 8:1984 [1994]). However, heterogeneous telomeric sequences have been reported in some organisms (e.g., the sequence TG<sub>1,3</sub> in *Saccharomyces*). In addition, the repeated telomeric sequence in some organisms is much longer, such as the 25 base pair sequence of *Kluyveromyces lactis*. Moreover, the telomeric structure of some organisms is completely different. For example, the telomeres of *Drosophila* are comprised of a transposable element (See, Biessman *et al.*, Cell 61:663 [1990]; and F.-m Sheen and Levis, Proc. Natl. Acad. Sci., 91:12510 [1994]).

The telomeric DNA sequences of many organisms have been determined (See e.g., Zakian, Science 270:1601 [1995]). However, it has been noted that as more telomeric sequences become known, it is becoming increasingly difficult to identify even a loose consensus sequence to describe them (Zakian, *supra*). Furthermore, it is known that the average amount of telomeric DNA varies between organisms. For example, mice may have as many as 150 kb (kilobases) of telomeric DNA per telomere, while the telomeres of *Oxytricha* macronuclear DNA molecules are only 20 bp in length (Kipling and Cooke, Nature 347:400 [1990]; Starling *et al.*, Nucleic Acids Res., 18:6881 [1990]; and Klobutcher *et al.*, Proc. Natl. Acad. Sci., 78:3015 [1981]). Moreover, in most organisms, the amount of telomeric DNA fluctuates. For example, the amount of telomeric DNA at individual yeast telomeres in a wild-type strain may range from approximately 200 to 400 bp, with this amount of DNA increasing and decreasing stochastically (Shampay and Blackburn, Proc. Natl. Acad. Sci., 85:534 [1988]). Heterogeneity and spontaneous changes in telomere length may reflect a complex balance between the processes involved in degradation and lengthening of telomeric tracts. In addition, genetic, nutritional and other factors may cause increases or decreases in telomeric length (Lustig and Petes, Natl. Acad. Sci., 83:1398 [1986]; and Sandell *et al.*, Cell 91:12061 [1994]). The inherent heterogeneity of virtually all



telomeric DNAs suggests that telomeres are not maintained via conventional replicative processes.

In addition to the telomeres themselves, the regions located adjacent to telomeres have been studied. For example, in most organisms, the sub-telomeric regions immediately internal to the simple repeats consist of middle repetitive sequences, designated as telomere-associated ("TA") DNA. These regions bear some similarity with the transposon telomeres of *Drosophila*. In *Saccharomyces*, two classes of TA elements, designated as "X" and "Y," have been described (Chan and Tye, Cell 33:563 [1983]). These elements may be found alone or in combination on most or all telomeres.

#### **Telomeric Structural Proteins**

Various structural proteins that interact with telomeric DNA have been described which are distinct from the protein components of the telomerase enzyme. Such structural proteins comprise the "telosome" of *Saccharomyces* chromosomes (Wright *et al.*, Genes Develop., 6:197 [1992]) and of ciliate macronuclear DNA molecules (Gottschling and Cech, Cell 38:501 [1984]; and Blackburn and Chiou, Proc. Natl. Acad. Sci., 78:2263 [1981]). The telosome is a non-nucleosomal, but discrete, chromatin structure that encompasses the entire terminal array of telomeric repeats. In *Saccharomyces*, the DNA adjacent to the telosome is packaged into nucleosomes. However, these nucleosomes are reported to differ from those in most other regions of the yeast genome, as they have features that are characteristic of transcriptionally inactive chromatin (Wright *et al.*, Genes Develop., 6:197 [1992]; and Braunstein *et al.*, Genes Develop., 7:592 [1993]). In mammals, most of the simple repeated telomeric DNA is packaged in closely spaced nucleosomes (Makarov *et al.*, Cell 73:775 [1993]; and Tommerup *et al.*, Mol. Cell. Biol., 14:5777 [1994]). However, the telomeric repeats located at the very ends of the human chromosomes are found in a telosome-like structure.

#### **Telomere Replication**

Complete replication of the ends of linear eukaryotic chromosomes presents special problems for conventional methods of DNA replication. For example,

conventional DNA polymerases cannot begin DNA synthesis *de novo*, rather, they require RNA primers which are later removed during replication. In the case of telomeres, removal of the RNA primer from the lagging-strand end would necessarily leave a 5'-terminal gap, resulting in the loss of sequence if the parental telomere was blunt-ended (Watson, *Nature New Biol.*, 239:197 [1972]; Olovnikov, *J. Theor. Biol.*, 41:181 [1973]). However, the described telomeres have 3' overhangs (Klobutcher *et al.*, *Proc. Natl. Acad. Sci.*, 58:3015 [1981]; Henderson and Blackburn, *Mol. Cell. Biol.*, 9:345 [1989]; and Wellinger *et al.*, *Cell* 72:51 [1993]). For these molecules, it is possible that removal of the lagging-strand 5'-terminal RNA primer could regenerate the 3' overhang without loss of sequence on this side of the molecule. However, loss of sequence information on the leading-strand end would occur, because of the lack of a complementary strand to act as template in the synthesis of a 3' overhang (Zahler and Prescott, *Nucleic Acids Res.*, 16:6953 [1988]; Lingner *et al.*, *Science* 269:1533 [1995]).

Nonetheless, complete replication of the chromosomes must occur. While conventional DNA polymerases cannot accurately reproduce chromosomal DNA ends, specialized factors exist to ensure their complete replication. Telomerase is a key component in this process. Telomerase is a ribonucleoprotein (RNP) particle and polymerase that uses a portion of its internal RNA moiety as a template for telomere repeat DNA synthesis (U.S. Patent No. 5,583,016; Yu *et al.*, *Nature* 344:126 [1990]; Singer and Gottschling, *Science* 266:404 [1994]; Autexier and Greider, *Genes Develop.*, 8:563 [1994]; Gilley *et al.*, *Genes Develop.*, 9:2214 [1995]; McEachern and Blackburn, *Nature* 367:403 [1995]; Blackburn, *Ann. Rev. Biochem.*, 61:113 [1992]; Greider, *Ann. Rev. Biochem.*, 65:337 [1996]). The activity of this enzyme depends upon both its RNA and protein components to circumvent the problems presented by end replication by using RNA (*i.e.*, as opposed to DNA) to template the synthesis of telomeric DNA. Telomerases extend the G strand of telomeric DNA. A combination of factors, including telomerase processivity, frequency of action at individual telomeres, and the rate of degradation of telomeric DNA, contribute to the size of the telomeres (*i.e.*, whether they are lengthened, shortened, or maintained at a certain size). *In vitro*, telomerases may be extremely processive, with the *Tetrahymena* telomerase

adding an average of approximately 500 bases to the G strand primer before dissociation of the enzyme (Greider, Mol. Cell. Biol., 11:4572 [1991]).

Importantly, telomere replication is regulated both by developmental and cell cycle factors. It has been hypothesized that aspects of telomere replication may act as signals in the cell cycle. For example, certain DNA structures or DNA-protein complex formations may act as a checkpoint to indicate that chromosomal replication has been completed (See e.g., Wellinger *et al.*, Mol. Cell. Biol., 13:4057 [1993]). In addition, it has been observed that, in humans, telomerase activity is not detectable in most somatic tissues, although it is detected in many tumors (U.S. Patent No. 5,583,016, *supra*). Thus, telomere length is believed serve as a mitotic clock, which limits the replication potential of cells *in vivo* and/or *in vitro*. What remains needed in the art are additional methods to study the role of telomeres and their replication in normal as well as abnormal cells (*i.e.*, cancerous cells). An understanding of telomerase and its function is needed to develop better means for use of telomerase as a target for cancer therapy or anti-aging processes.

### SUMMARY OF THE INVENTION

This invention has for the first time provided for the cloning, characterization, synthesis, purification and recombinant expression of a genus of TRT enzymes and telomerase enzyme complexes including, also for the first time, the important human telomerase reverse transcriptase protein (hTRT), as well as novel methods and reagents complementing this significant achievement.

The present invention provides compositions and methods for purification and use of telomerase. In particular, the present invention is directed to telomerase and co-purifying polypeptides obtained from *Euplotes aediculatus*, as well as other organisms (*e.g.*, *Schizosaccharomyces*, other yeast, *Tetrahymena*, other fungi, mouse and other mammals). The present invention also provides methods useful for the detection and identification of telomerase homologs in other species and genera of organisms.

The present invention relates to the cloning and characterization of the catalytic protein component of telomerase, referred to as telomerase reverse transcriptase

("TRT"). In one aspect, the present invention provides TRT genes and proteins from ciliates, fungi, and vertebrates, especially mammals. In one important aspect, the present invention relates to the cloning and characterization of the catalytic protein component of human telomerase ("hTRT").

5           In one aspect, the present invention provides reagents and methods for identifying and cloning novel TRTs using: nucleic acid probes and primers generated or derived from the TRT polynucleotides for cloning TRT genes and cDNAs; and, antibodies that specifically recognize TRTs, including the motifs or other TRT epitopes, and such antibodies are useful for expression cloning of TRT genes,  
10       identification and purification of the genus of TRT polypeptides, and other applications as disclosed herein.

          The present invention provides heretofore unknown telomerase TRT subunit proteins of *E. aediculatus* of approximately 123 kDa (SEQ ID NO:2) and 43 kDa (SEQ ID NO:4-6), as measured on SDS-PAGE. In particular, the present invention provides  
15       substantially purified *E. aediculatus* 123 kDa and 43 kDa telomerase protein subunits.

          One aspect of the invention features isolated and substantially purified polynucleotides which encode telomerase subunits (*i.e.*, the *E. aediculatus* 123 kDa and 43 kDa protein subunits). In a particular aspect, the polynucleotide is the *E. aediculatus* nucleotide sequence of SEQ ID NO:1 (DNA sequence of the *E. aediculatus*  
20       telomerase gene encoding the 123 kDa telomerase protein subunit), or variants thereof. In an alternative embodiment, the present invention provides fragments of the isolated (*i.e.*, substantially purified) polynucleotide encoding the *E. aediculatus* telomerase 123 kDa subunit of at least 10 amino acid residues in length. The invention further contemplates fragments of this polynucleotide sequence (*i.e.*, SEQ ID NO:1) that are at  
25       least 6 nucleotides, at least 25 nucleotides, at least 30 nucleotides, at least 100 nucleotides, at least 250 nucleotides, and at least 500 nucleotides in length. In addition, the invention features polynucleotide sequences that hybridize under stringent conditions to SEQ ID NO:1, or fragments thereof. The present invention further contemplates a polynucleotide sequence comprising the complement of the nucleic acid  
30       of SEQ ID NO:1, or variants thereof.

The present invention also provides the polynucleotide with the sequence of SEQ ID NO:3 ( DNA sequence of the gene encoding the *E. aediculatus* 43 kDa telomerase protein subunit). In particular, the present invention provides the polynucleotide sequence comprising at least a portion of the nucleic acid sequence of SEQ ID NO:3, or variants, thereof. In one embodiment, the present invention provides fragments of the isolated (*i.e.*, substantially purified) polynucleotide encoding the *E. aediculatus* telomerase 43 kDa subunit of at least 10 amino acid residues in length. The invention also provides an isolated polynucleotide sequence encoding the *E. aediculatus* polypeptide of SEQ ID NOS:4-6 (the amino acid sequences of all three open reading frames of the *E. aediculatus* 43 kDa telomerase protein subunit), or variants thereof. The invention further contemplates fragments of this polynucleotide sequence (*i.e.*, SEQ ID NO:3) that are at least 5 nucleotides, at least 20 nucleotides, at least 100 nucleotides, at least 250 nucleotides, and at least 500 nucleotides in length. In addition, the invention features polynucleotide sequences that hybridize under stringent conditions to SEQ ID NO:3, or fragments thereof. The present invention further contemplates a polynucleotide sequence comprising the complement of the nucleic acid of SEQ ID NO:3, or variants thereof.

The present invention provides a substantially purified *E. aediculatus* polypeptide comprising at least a portion of the amino acid sequence of SEQ ID NO:2 (123 kDa *E. aediculatus* telomerase TRT subunit), or variants thereof. In one embodiment, the portion of the polypeptide sequence comprises fragments of SEQ ID NO:2, having a length greater than 10 amino acids. However, the invention also contemplates polypeptide sequences of various lengths, the sequences of which are included within SEQ ID NO:2, ranging from 5-500 amino acids. The present invention also provides an isolated polynucleotide sequence encoding the polypeptide of SEQ ID NO:2, or variants, thereof.

The present invention provides a substantially purified *E. aediculatus* polypeptide comprising at least a portion of the amino acid sequence selected from the group consisting of SEQ ID NO:4-6 (open reading frames of the *E. aediculatus* 43 kDa telomerase protein subunit), or variants thereof. In one embodiment, the portion of the

polypeptide comprises fragments of SEQ ID NO:4, having a length greater than 10 amino acids. In an alternative embodiment, the portion of the polypeptide comprises fragments of SEQ ID NO:5, having a length greater than 10 amino acids. In yet another alternative embodiment, the portion of the polypeptide comprises fragments of SEQ ID NO:6, having a length greater than 10 amino acids. The present invention also contemplates polypeptide sequences of various lengths, the sequences of which are included within SEQ ID NOS:4, 5, and/or 6 (*Euplotes aediculatus* 43 kDa polypeptide open reading frames shown in SEQ ID NOS:4-6), ranging from 5 to 500 amino acids.

The present invention also provides a telomerase complex comprised of at least one purified recombinant *E. aediculatus* 123 kDa telomerase protein subunit, at least one purified recombinant *E. aediculatus* 43 kDa telomerase protein subunit, and purified recombinant RNA. In a preferred embodiment, the telomerase complex comprises one purified recombinant 123 kDa telomerase protein subunit, one purified recombinant 43 kDa telomerase protein subunit, and purified recombinant telomerase RNA. In one preferred embodiment, the telomerase complex comprises an 123 kDa and/or telomerase protein subunit obtained from *Euplotes aediculatus*. It is contemplated that the 123 kDa telomerase protein subunit of the *E. aediculatus* telomerase complex can be encoded by SEQ ID NO:1. It is also contemplated that the 123 kDa *E. aediculatus* telomerase protein subunit of the telomerase complex be comprised of amino acids as shown in SEQ ID NO:2. It is also contemplated that the 43 kDa telomerase protein subunit of the telomerase complex can be obtained by purification from *E. aediculatus*. It is further contemplated that the 43 kDa telomerase subunit of the telomerase complex can be encoded by SEQ ID NO:3. It is also contemplated that the 43 kDa telomerase protein subunit of the telomerase complex be comprised of amino acids in the sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6. It is contemplated that the purified RNA of the telomerase complex be comprised of the RNA encoded by such sequences as those disclosed by Linger *et al.*, (Lingner *et al.*, Genes Develop., 8:1985 [1994]). In a preferred embodiment, the telomerase complex is capable of replicating telomeric DNA.

The present invention also provides methods for identifying a genus of TRTs and telomerase protein subunits in eukaryotic organisms other than *E. aediculatus*. These methods are comprised of multiple steps. The first step is the synthesis of at least one probe or primer oligonucleotide that encodes (is identical or complementary to) at least a portion of a known TRT coding sequence, such as a portion of the coding sequence for the amino acid sequence of SEQ ID NOS:2, 4, 5, or 6. In the alternative, the synthesized probe or primer oligonucleotides are complementary to at least a portion of the *E. aediculatus* coding sequence for the amino acid sequence of SEQ ID NO:2, 4, 5, or 6. The next step comprises exposing at least one of the probe or primer oligonucleotide(s) to nucleic acid from the genome or, in the alternative, the expressed portion of the genome of the other organism (*i.e.*, the non-*E. aediculatus* organism), under conditions suitable for the formation of nucleic acid hybrids. Next, the hybrids are identified with or without amplification, such as by probe labeling or by using a DNA polymerase (*e.g.*, *Taq*, or any other suitable polymerase known in the art) for amplification. Finally, the sequence of the hybrids are determined using methods known in the art, and the sequences of the derived amino acid sequences analyzed for their similarity to SEQ ID NOS:2, 4, 5, or 6.

The present invention also provides methods for identifying any member of the genus of nucleic acid sequences encoding telomerase protein subunits in eukaryotic organisms comprising the steps of: providing a sample believed to contain nucleic acid encoding an eukaryotic telomerase protein subunit; contacting the same with at least one oligonucleotide primer identical or complementary to the nucleic acid sequence encoding at least a region of a known TRT, such as an *Euplotes aediculatus* telomerase protein subunit and a polymerase; incubating under conditions such that the nucleic acid encoding the eukaryotic telomerase protein subunit is amplified by primer extension; determining the sequence of the eukaryotic telomerase protein subunit; and comparing the sequence of the eukaryotic telomerase protein subunit and the *Euplotes aediculatus* telomerase protein subunit. In one preferred embodiment, the *Euplotes aediculatus* telomerase subunit comprises at least a portion of SEQ ID NO:1. In an

alternative preferred embodiment, the *Euplotes aediculatus* telomerase subunit comprises at least a portion of SEQ ID NO:3.

Thus, the present invention also provides methods for identification of telomerase protein subunits in eukaryotic organisms other than *E. aediculatus*. The present invention allows one to compare the *E. aediculatus* amino acid sequences of SEQ ID NOS:2, 4, 5, or 6, and amino acid sequences derived from gene sequences of other organisms or obtained by direct amino acid sequence analysis of protein. The amino acid sequences shown to have the greatest degree of identity (*i.e.*, homology) to SEQ ID NOS:2, 4, 5, or 6, can then be selected for further testing. Sequences of particular importance are those that share identity with the reverse transcriptase (RT) or other motifs characteristic of the *Euplotes* sequence. Once identified, the proteins with the sequences showing the greatest degree of identity may be tested for their role in telomerase activity by genetic or biochemical methods, including the methods set forth in the Examples below.

The present invention also provides methods for purification of the TRT genus of the invention comprising the steps of providing a sample containing; exposing the sample to an affinity oligonucleotide under conditions wherein the affinity oligonucleotide binds to the telomerase to form a telomerase-oligonucleotide complex; and exposing the oligonucleotide-telomerase complex to a displacement oligonucleotide under conditions such that the telomerase is released from the template. In a preferred embodiment, the method comprises the further step of eluting the telomerase. In another preferred embodiment, the affinity oligonucleotide comprises an antisense portion and a biotin residue. It is contemplated that, in one embodiment, during the exposing step, a biotin residue on the affinity oligonucleotide binds to an avidin bead and the antisense portion binds to the telomerase. It is also contemplated that, during the exposing step, the displacement oligonucleotide binds to the affinity oligonucleotide.

The present invention further provides substantially purified polypeptides comprising the amino acid sequence comprising SEQ ID NOS: 58 (*Oxytricha*), 61 (human telomerase motifs), 63 (*Schizosaccharomyces pombe*), 64 (*S. cerevisiae*), 65



(*Euplotes aediculatus*), 67 (human telomerase motifs), and 68 (*Schizosaccharomyces*).

In another embodiment, the present invention also provides purified, isolated polynucleotide sequences encoding the polypeptides comprising the amino acid sequences of SEQ ID NOS:58, 61, 63, 64, 65, 67, and 68. The present invention  
5 contemplates that the oligonucleotides may encode (or be identical or complementary to) any portion of a sequence that encodes portions or fragments of SEQ ID NOS:58, 61, 63, 64, 65, 67, and 68, of various lengths. In one embodiment, the portion of the polypeptide, including fragments of lengths greater than about 5, 10 or more amino acids. However, the present invention also contemplates polynucleotides that encode  
10 and the polypeptides encoded of sequences of various lengths, the sequences of which are included within SEQ ID NOS:58, 61, 63, 64, 65, 67, and 68, ranging from 5 to 500 amino acids (as appropriate, based on the length of SEQ ID NOS:58, 61, 63, 64, 65, 67, and 68).

The present invention also provides nucleic acid sequences identical,  
15 complementary to or comprising SEQ ID NOS:55 (*S. cerevisiae*), 62 (human telomerase motifs), 66 (*S. cerevisiae*), and 69 (*Schizosaccharomyces*), or variants thereof. The present invention further provides fragments of the isolated polynucleotide sequences that are at least 6 nucleotides, at least 10, at least 20, at least 25 nucleotides, at least 30 nucleotides, at least 50 nucleotides, at least 100 nucleotides,  
20 at least 250 nucleotides, and at least 500 nucleotides in length (as appropriate for the length of the sequence of SEQ ID NOS:55, 62, 66, and 69, or variants thereof and the intended application).

In particularly preferred embodiments, the polynucleotide hybridizes specifically to an individual species of the genus of TRT telomerase sequences, wherein  
25 the telomerase sequences are selected from the group consisting of mammalian (*i.e.*, human, mouse), *Euplotes aediculatus*, *Oxytricha*, *Schizosaccharomyces*, and *Saccharomyces* telomerase sequences. In other preferred embodiments, the present invention provides polynucleotide sequences comprising the complement of nucleic acid sequences selected from the group consisting of SEQ ID NOS:55, 62, 66, and 69,  
30 or variants thereof. In yet other preferred embodiments, the present invention provides

polynucleic acid sequences that hybridize under stringent conditions to at least one nucleic acid sequence selected from the group consisting of SEQ ID NO:55, 62, 66, and 69. In a further embodiment, the polynucleotide sequence comprises a purified, synthetic nucleotide sequence having a length of about ten to thirty nucleotides.

5 In alternative preferred embodiments, the present invention provides polynucleotide sequences corresponding to hTERT, the human telomerase, including SEQ ID NOS:113 and 117 (human), and their complementary sequences. The invention further contemplates fragments of these polynucleotide sequence (*i.e.*, SEQ ID NOS:113, and 117) that are at least 5 nucleotides, at least 20 nucleotides, at least 100 nucleotides, at least 250 nucleotides, and at least 500 nucleotides in length. The invention further contemplates fragments of the complements of these polynucleotide sequences (*i.e.*, SEQ ID NOS:113, and 117) that are at least 5 nucleotides, at least 20 nucleotides, at least 100 nucleotides, at least 250 nucleotides, and at least 500 nucleotides in length. In addition, the invention features polynucleotide sequences that 15 hybridize under stringent conditions to SEQ ID NOS:113 and 117, and/or fragments, and/or the complementary sequences thereof. The present invention further contemplates a polynucleotide sequence comprising the complement of the nucleic acids of SEQ ID NOS:113 and 117, or variants thereof. In a further embodiment, the polynucleotide sequence comprises a purified, synthetic nucleotide sequence 20 corresponding to a fragment of SEQ ID NOS:113 and/or 117, having a length of about ten to thirty nucleotides. The present invention further provides plasmid pGRN121 (ATCC accession # 209016), and the lambda clones 25-1.1 (ATCC accession # 209024) and GM5 (ATCC accession # 98505).

The present invention further provides substantially purified hTERT polypeptides 25 comprising the amino acid sequence comprising SEQ ID NOS:114-116, and 118 (human). In another embodiment, the present invention also provides purified, isolated polynucleotide sequences encoding the polypeptides comprising the amino acid sequences of SEQ ID NOS:114-116, and 118. The present invention contemplates portions or fragments of SEQ ID NOS:114-116, and 118, of various lengths. In one 30 embodiment, the portion of polypeptide comprises fragments of lengths greater than 10

amino acids. However, the present invention also contemplates polypeptide sequences of various lengths, the sequences of which are included within SEQ ID NOS:114-116, and 118, ranging from 5 to 1100 amino acids (as appropriate, based on the length of SEQ ID NOS:114-116, and 118).

5           The present invention also provides methods for detecting the presence of nucleotide sequences encoding at least a portion of a TRT in a biological sample, comprising the steps of, providing: a biological sample suspected of containing nucleic acid corresponding to the nucleotide sequence of a TRT, for example, as set forth in SEQ ID NOS:1 (*Euplotes*), 3 (*Euplotes*), 53 (*Tetrahymena*), 62 (human), 66 (*S.*  
10 *cerevisiae*), 69 (*Schizosaccharomyces*), 117 (human); the nucleotide of SEQ ID NO:1, 3, 53, 62, 66, 69, 117 or fragment(s) thereof; combining the biological sample with the nucleotide under conditions such that a hybridization complex is formed between the nucleic acid and the nucleotide; and detecting the hybridization complex.

          In one embodiment of the method, the nucleic acid corresponding to the  
15 nucleotide sequence of a TRT, for example, as set forth in SEQ ID NOS:1, 3, 53, 62, 66, 69, 117, is ribonucleic acid, while in an alternative embodiment, the nucleotide sequence is deoxyribonucleic acid. In yet another embodiment of the method, the detected hybridization complex correlates with expression of the polynucleotide of a TRT, for example, as set forth in SEQ ID NOS:1, 3, 53, 62, 66, 69, 117, in the  
20 biological sample. In yet another embodiment of the method, detection of the hybridization complex comprises conditions that permit the detection of nucleic acids with alterations, as compared to the polynucleotide of a TRT, for example, as set forth in SEQ ID NOS:1, 3, 53, 62, 66, 69, 117, in the biological sample.

          The present invention also provides antisense molecules comprising the nucleic  
25 acid sequence complementary to at least a portion of a TRT polynucleotide, for example, as set forth in SEQ ID NO:1, 3, 55, 62, 66, 67, 69 and 117. In an alternatively preferred embodiment, the present invention also provides pharmaceutical compositions comprising antisense molecules of SEQ ID NO:1, 3, 55, 62, 66, 67, 69 and 117, and a pharmaceutically acceptable excipient and/or other compound (*e.g.*  
30 adjuvant).

In yet another embodiment, the present invention provides TRT polynucleotide sequences contained on recombinant expression vectors. In one embodiment, the expression vector containing a TRT polynucleotide sequence is contained within a host cell.

5       The present invention also provides methods for producing TRT polypeptides comprising, for example, amino acid sequences as shown in SEQ ID NOS:2 (*Euplotes*), 4-6 (*Euplotes*), 52 (*Tetrahymena*), 58 (*Oxytricha*), 61 (human), 63 (*Schizosaccharomyces*), 64 (*S. cerevisiae*), 65 (*Euplotes*), 67 (human), 68 (*Schizosaccharomyces*), or 118 (human), the method comprising the steps of: culturing  
10 a host cell under conditions suitable for the expression of the TRT polypeptide; and recovering or purifying the polypeptide from the host cell culture.

      The present invention also provides purified antibodies that bind specifically to a polypeptide comprising at least a portion of the amino acid sequence of a TRT specie, including, for example, as shown in SEQ ID NOS:2, 4-6, 52, 58, 61, 63, 64, 65, 67, 68  
15 and/or 118. In one embodiment, the present invention provides a pharmaceutical composition comprising at least one antibody, and a pharmaceutically acceptable excipient.

      The present invention further provides methods for the detection of a TRT in a biological sample comprising the steps of: providing a biological sample suspected of  
20 expressing human telomerase protein; and at least one antibody that binds specifically to at least a portion of an amino acid sequence of a TRT, for example, as shown in SEQ ID NOS:2, 4-6, 52, 55, 61, 63, 64, 65, 67, 68 and/or 118; combining the biological sample and antibody(ies) under conditions such that an antibody:protein complex is formed; and detecting the complex wherein the presence of the complex correlates with  
25 the expression of the protein in the biological sample.

      The present invention further provides substantially purified peptides of TRT species, including, for example, peptides comprising all or a portion of the amino acid sequence selected from the group consisting of SEQ ID NOS:71, 73, 75, 77, 79, 82 (all  
30 *Tetrahymena*), 83 (*S. cerevisiae*), 84 (*Euplotes*), 85 (*Tetrahymena*), 86, and 101 (human). In an alternative embodiment, the present invention provides purified,

isolated polynucleotide sequences encoding the polypeptides corresponding to these sequences. In preferred embodiments, the polynucleotide hybridizes specifically to TRT sequences, wherein the TRT sequences are selected from the group consisting of mammalian (*e.g.*, human, mouse), *Euplotes aediculatus*, *Oxytricha*,  
5 *Schizosaccharomyces*, *Saccharomyces* and *Tetrahymena* sequences. In yet another embodiment, the polynucleotide sequence comprises the complement of a nucleic acid sequence selected from the group consisting of SEQ ID NOS:70, 72, 74, 76, 78, 80, 81 (all *Tetrahymena*), 100 (hTRT), 113 (hTRT), 117 (hTRT), and variants thereof. In a further embodiment, the polynucleotide sequence that hybridizes under stringent  
10 conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS:66 (*S. cerevisiae*), 69 (*Schizosaccharomyces*), 80 (*Tetrahymena*), and 81 (*Tetrahymena*). In yet another embodiment, the polynucleotide sequence is selected from the group consisting of: SEQ ID NOS:70, 72, 74, 76, 78 (all *Tetrahymena*); 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 (all hTRT); 102, 103, 104, 105, 106 (all *S.*  
15 *pombe*); 107 (Adapt Sfil), 108 (Adapt SfII), 109 (*S. pombe*), 110 (*S. pombe*), 111 (*Tetrahymena*), 113 (hTRT), and 117 (hTRT). In an alternative embodiment, the nucleotide sequence comprises a purified, synthetic nucleotide sequence having a length of about ten to fifty nucleotides.

The present invention also provides methods for detecting the presence of  
20 nucleotide sequences encoding at least a portion of a TRT in a biological sample, comprising the steps of, providing: a biological sample suspected of containing nucleic acid corresponding to the nucleotide sequence of a TRT, for example, as shown in SEQ ID NO:100, and/or SEQ ID NO:113, and/or SEQ ID NO:117; the nucleotide of SEQ ID NO:100, and/or SEQ ID NO:113, and/or SEQ ID NO:117, or fragment(s) thereof;  
25 combining the biological sample with the nucleotide under conditions such that a hybridization complex is formed between the nucleic acid and the nucleotide; and detecting the hybridization complex.

In one embodiment of the method, the TRT nucleic acid corresponding to the nucleotide sequence of SEQ ID NO:100, and/or SEQ ID NO:113, and/or SEQ ID  
30 NO:117, is ribonucleic acid, while in an alternative embodiment, the nucleotide

sequence is deoxyribonucleic acid. In yet another embodiment of the method, the detected hybridization complex correlates with expression of the polynucleotide of SEQ ID NO:100, and/or SEQ ID NO:113, and/or SEQ ID NO:117, in the biological sample. In yet another embodiment of the method, detection of the hybridization  
5 complex comprises incubation under conditions that permit the detection of alterations in the nucleic acid, as compared to the polynucleotide of SEQ ID NO:100 and/or SEQ ID NO:113, and/or SEQ ID NO:117, in the biological sample.

The present invention also provides antisense molecules comprising nucleic acid sequences, for example, complementary to at least a portion of TRT  
10 polynucleotides, including, for example, as shown in SEQ ID NO:82 (*Tetrahymena*), 100, 113, and 117 (all hTRT). In an alternatively preferred embodiment, the present invention also provides pharmaceutical compositions comprising antisense molecules of SEQ ID NOS:82, 100, 113, 117, and a pharmaceutically acceptable excipient and/or other compound (*e.g.*, adjuvant).

15 In yet another embodiment, the present invention provides TRT polynucleotide sequences contained in recombinant expression vectors. In one embodiment, the expression vector containing the polynucleotide sequence is contained within a host cell.

The present invention also provides methods for producing TRT polypeptides  
20 comprising, for example, the amino acid sequence of SEQ ID NOS:82, 83, 84, 85, 86, 101, 114, 115, 116, and/or 118, the method comprising the steps of: culturing a host cell under conditions suitable for the expression of the polypeptide; and recovering or purifying the polypeptide from the host cell culture.

The present invention also provides purified antibodies that binds specifically to  
25 a TRT polypeptide comprising at least a portion of the TRT amino acid sequence of, for example, SEQ ID NOS:2, 2-4, 71, 73, 75, 77, 79, 82, 83, 84, 85, 86, 101, 114, 115, 116, and/or 118. In one embodiment, the present invention provides a pharmaceutical composition comprising at least one antibody, and a pharmaceutically acceptable excipient.

The present invention further provides methods for the detection of TRT in a biological sample comprising the steps of: providing a biological sample suspected of expressing TRT protein; and at least one antibody that binds specifically to at least a portion of the amino acid sequence of the TRT, for example, SEQ ID NOS:71, 73, 75,  
5 77, 79, 82, 83, 84, 85, 86, 87, 101, 114, 115, 116, and/or 118, combining the biological sample and antibody(ies) under conditions such that an antibody:protein complex is formed; and detecting the complex wherein the presence of the complex correlates with the expression of the telomerase in the biological sample.

The present invention provides a purified telomerase complex comprised of at  
10 least one TRT, a telomerase-associated nucleic acid moiety used as a template for telomere repeat DNA synthesis, and optionally other telomerase enzyme complex-associated proteins, such as co-purifying proteins and other proteins that regulate enzyme activity. In one embodiment, the telomerase enzyme complex is comprised of components of human origin, including human telomerase enzyme (comprising hTERT,  
15 encoded by the cDNA of SEQ ID NO:117), a human telomerase RNA (hTR) moiety and telomerase-associated proteins. In one embodiment, the complex comprises an hTERT protein of about 127 kd, having the sequence of SEQ ID NO:118, encoded by the cDNA SEQ ID NO:117.

The present invention also provides a number of different methods for  
20 expressing and isolating telomerase and telomerase-associated compounds that can be employed, in one or more aspects, as reagents and methodologies.

The methods and reagents of the present invention provide TRT genes and sequences that can be used to knock out homologous genes in cells. The novel reagents and methods of the invention thus provide TRT knockout cells and animals and  
25 methods for making such cells and transgenic mammals.

One aspect of the invention is the use of a polynucleotide that is at least ten nucleotides to about 10 kb or more in length and comprises a contiguous sequence of at least ten nucleotides that is identical or exactly complementary to a contiguous sequence in a naturally occurring TRT gene or TRT mRNA in assaying or screening for an TRT  
30 gene sequence or TRT mRNA, or in preparing a recombinant host cell.

A further aspect of the invention is the use of an agent increasing expression of TRT in the manufacture of a medicament for the treatment of a condition addressed by increasing proliferative capacity of a vertebrate cell, optionally the medicament being for inhibiting the effects of ageing.

5 Yet a further aspect of the invention is the use of an inhibitor of telomerase activity in the manufacture of a medicament for the treatment of a condition associated with an elevated level of telomerase activity within a human cell.

The proteins, variants and fragments of the invention, and the encoding polynucleotides or fragments, are also each provided in a further aspect of this invention  
10 for use as a pharmaceutical.

The invention further includes the use of a protein, variant or fragment, or of a polynucleotide or fragment, in each case as defined herein, in the manufacture of a medicament, for example in the manufacture of a medicament for inhibiting an effect of aging or cancer.

15 In certain embodiments of the present invention, the TRT polynucleotides are other than the 389 nucleotide polynucleotide of AA281296 (SEQ ID NO:121) and/or other than clone 712562, the plasmid containing an insert, the sequence of which insert is shown in Figure 58, SEQ ID NO:122.

The invention further includes the use of a protein, variant or fragment, or of a  
20 polynucleotide or fragment, in each case as defined herein, in the manufacture of a medicament, for example in the manufacture of a medicament for inhibiting an effect of aging or cancer. Another aspect of the invention is a polynucleotide selected from:  
(a) the DNA having a sequence as set forth in SEQ ID NOS:2, 4-6, 52, 58, 61, 63, 64, 65, 67, 68, or 117; (b) a polynucleotide of at least 10 nucleotides which hybridizes to the  
25 foregoing DNA and which codes for an hTRT protein or variant or which hybridizes to a coding sequence for such a variant; and, (c) DNA sequences which are degenerate as a result of the genetic code to the DNA sequences defined in (a) and (b) and which code for an hTRT polypeptide or variant.



### DESCRIPTION OF THE FIGURES

Figure 1 is a schematic diagram of the affinity purification of telomerase showing the binding and displacement elution steps.

Figure 2 is a photograph of a Northern blot of telomerase preparations obtained during purification of *Euplotes* telomerase.

Figure 3 shows telomerase activity through the *Euplotes* telomerase purification protocol.

Figure 4 is a photograph of a SDS-PAGE gel of *Euplotes* telomerase, showing the presence of an approximately 123 kDa polypeptide and an approximately 43 kDa doublet.

Figure 5 is a graph showing the sedimentation coefficient of *Euplotes* telomerase.

Figure 6 is a photograph of a polyacrylamide/urea gel with 36% formamide containing *Euplotes* telomerase.

Figure 7 shows the putative alignments of a telomerase RNA template, with SEQ ID NOS:43 and 44 in Panel A, and SEQ ID NOS:45 and 46 in Panel B.

Figure 8 is a photograph of lanes 25-30 of the gel shown in Figure 6, shown at a lighter exposure level.

Figure 9 shows the DNA sequence of the *Euplotes* telomerase gene encoding the 123 kDa telomerase protein subunit (SEQ ID NO:1).

Figure 10 shows the amino acid sequence of the *Euplotes* 123 kDa telomerase protein subunit (SEQ ID NO:2).

Figure 11 shows the DNA sequence of the gene encoding the *Euplotes* 43 kDa telomerase protein subunit (SEQ ID NO:3).

Figure 12 shows the DNA sequence, as well as the amino acid sequences of all three open reading frames of the *Euplotes* 43 kDa telomerase protein subunit (SEQ ID NOS:4-6).

Figure 13 shows a sequence comparison between the 123 kDa telomerase protein subunit of *E. aediculatus* (positions 2 through 1008 of SEQ ID NO:2) and the 80 kDa polypeptide of *T. thermophila* (SEQ ID NO:52).

Figure 14 shows a sequence comparison between the 123 kDa telomerase protein subunit of *E. aediculatus* (positions 132 through 1028 of SEQ ID NO:2) and the 95 kDa polypeptide of *T. thermophila* (SEQ ID NO:54).

5 Figure 15 shows the best-fit alignment between a portion of the "La-domain" of the 43 kDa telomerase protein subunit of *E. aediculatus* (SEQ ID NO:9) and a portion of the 95 kDa polypeptide of *T. thermophila* (SEQ ID NO:10).

Figure 16 shows the best-fit alignment between a portion of the "La-domain" of the 43 kDa telomerase protein subunit of *E. aediculatus* (SEQ ID NO:11) and a portion of the 80 kDa polypeptide of *T. thermophila* (SEQ ID NO:12).

10 Figure 17 shows the alignment and motifs of the polymerase domain of the 123 kDa telomerase protein subunit of *E. aediculatus* (SEQ ID NOS:13 and 18) and the polymerase domains of various reverse transcriptases (RT) (SEQ ID NOS:14-17, and 19-22).

Figure 18 shows the alignment of a domain of the 43 kDa telomerase protein subunit (SEQ ID NO:23) with various La proteins (SEQ ID NOS:24-27).

15 Figure 19 shows the nucleotide sequence encoding the *T. thermophila* 80 kDa polypeptide (SEQ ID NO:51).

Figure 20 shows the amino acid sequence of the *T. thermophila* 80 kDa polypeptide (SEQ ID NO:52).

20 Figure 21 shows the nucleotide sequence encoding the *T. thermophila* 95 kDa polypeptide (SEQ ID NO:53).

Figure 22 shows the amino acid sequence of the *T. thermophila* 95 kDa polypeptide (SEQ ID NO:54).

25 Figure 23 shows the amino acid sequence of L8543.12 ("Est2p") (*Saccharomyces cerevisiae*) (SEQ ID NO:55).

Figure 24 shows the alignment of the amino acid sequence encoded by an *Oxytricha* PCR product (SEQ ID NO:58) with the *Euplotes* TRT sequence (SEQ ID NO:59).

30 Figure 25 shows the alignment of the hTRT amino acid motifs (SEQ ID NO:61), with portions of the *tez1 Schizosaccharomyces pombe* (*S. pombe*) sequence (SEQ ID

NO:63), *S. cerevisiae* Est2p (SEQ ID NO:64), and the *Euplotes* p123 (SEQ ID NO:65) amino acid sequences.

Figure 26 shows the DNA sequence of *S. cerevisiae* Est2 (SEQ ID NO:66).

Figure 27 shows the amino acid sequence (SEQ ID NO:67) encoded by the nucleic acid sequence of Figure 28 (SEQ ID NO:62).

Figure 28 shows the DNA sequence (SEQ ID NO:62) encoding the amino acid sequence of SEQ ID NO:67 of Figure 27, as shown in Figure 25 (SEQ ID NO:61).

Figure 29 shows the amino acid sequence of *Schizosaccharomyces tez1* (SEQ ID NO:68).

Figure 30 shows the DNA sequence of *Schizosaccharomyces tez1* ("Sp\_Trt1p") (SEQ ID NO:69).

Figure 31 shows the alignment of *S. cerevisiae* EST2p (SEQ ID NO:83), *Euplotes* (SEQ ID NO:84), and *Tetrahymena* (SEQ ID NO:85) amino acid sequences, as well as a consensus sequence.

Figure 32 shows sequences of peptides useful for production of anti-TRT antibodies.

Figure 33 is a schematic summary of the *S. pombe tez1*<sup>+</sup> sequencing experiments.

Figure 34 shows two degenerate PCR primers used to identify the *S. pombe* homolog of the *E. aediculatus* p123 sequences.

Figure 35 shows the four major bands produced in PCR using the degenerate primers shown in Figure 34.

Figure 36 shows the alignment of the amino acid sequence encoded by the M2 PCR product with *E. aediculatus* p123, *S. cerevisiae*, and *Oxytricha* (SEQ ID NO:58) TRT protein sequences.

Figure 37 is a schematic showing the 3' RT PCR strategy for obtaining *S. pombe* TRT sequences.

Figure 38 shows the libraries and the results of screening libraries for *S. pombe* telomerase protein sequences.

Figure 39 shows the results obtained with the *HindIII*-digested positive genomic clones containing *S. pombe* telomerase sequence.

Figure 40 is a schematic showing the 5' RT PCR strategy for obtaining *S. pombe* TRT sequences.

Figure 41 shows the alignment of RT domains from telomerase catalytic subunits.

Figure 42 shows the alignment of three telomerase sequences.

5        Figure 43 shows the disruption strategy used to disrupt the telomerase genes in *S. pombe*.

Figure 44 shows the experimental results confirming disruption of *Schizosaccharomyces pombe tez1*.

10        Figure 45 shows the progressive shortening of telomeres in *S. pombe* due to *tez1* disruption.

Figure 46 shows the DNA (SEQ ID NO:69) and amino acid (SEQ ID NO:68) sequence of *tez1*, with the coding regions indicated.

15        Figure 47 shows the DNA (SEQ ID NO:100) and encoded amino acid (SEQ ID NO:101) of the open reading frame (ORF) for the approximately 63 kDa telomerase protein or fragment thereof, from the EcoRI-NotI insert of clone 712562 (SEQ ID NO:122), which includes the Genbank #AA281296 EST (SEQ ID NO:121).

Figure 48 shows an alignment of reverse transcriptase motifs from various sources.

Figure 49 provides a restriction and function map of plasmid pGRN121 (ATCC accession # 209016).

20        Figure 50 provides the results of preliminary nucleic acid sequencing analysis of hTRT (SEQ ID NO:113).

Figure 51 provides a preliminary nucleic acid (SEQ ID NO:113) and deduced ORF sequence (SEQ ID NOS:114-116) of hTRT.

Figure 52 provides a refined restriction and function map of plasmid pGRN121.

25        Figure 53 provides the nucleic acid (SEQ ID NO:117) and deduced ORF sequence (SEQ ID NO:118) of hTRT.

Figure 54 provides a restriction map of lambda clone 25-1.1 (ATCC accession # 209024).

30        Figure 55 shows a multiple sequence alignment of TRT consensus sequences, *i.e.*, motifs ("TRT con") with TRT sequences from several species of the TRT genus,

including: *S. pombe* Trt1 ("Sp\_Trt1p"); human TRT ("hTRT"); *Euplotes* p123 ("EA\_p123"); and *Saccharomyces cerevisiae* Est2p (Sc\_Est2p"). Figure 55 also shows a multiple sequence alignment of reverse transcriptase consensus sequences, *i.e.*, RT motifs ("RT con") and consensus sequences from other RT motif-containing proteins including:

5 "Sc\_a1", cytochrome oxidase group II intron 1-encoded protein from *S. cerevisiae* mitochondria; "Bm\_R1", reverse transcriptase from *Bombyx mori* R1 non-LTR retrotransposable element; and reverse transcriptase from HIV-1.

Figure 56 shows the alignment of mouse telomerase reverse transcriptase protein (mTRT) with hTRT.

10 Figure 57 shows a comparison and alignment of hTRT; *S. pombe* Trt1 ("spTRT"); *Euplotes* p123 ("eaTRT"); and *S. cerevisiae* EST2p TRT sequence ("sc\_Est2"). The figure also shows a comparison of TRT consensus sequences, *i.e.*, conserved TRT motif sequences ("TRT con"), with these sequences; comparing in Figure 57A motifs designated "Telomerase Specific Motifs"; in Figure 57B "Telomerase RT Motifs (Fingers)"; and in

15 Figure 57C "Telomerase RT Motifs (Palm, Primer Grip)."

Figure 58 shows a preliminary nucleic acid and amino acid sequence analysis of hTRT (designated SEQ ID NO:119 and 120, respectively).

Figure 59 shows the complete sequencing of the TRT cDNA of clone #712562 (SEQ ID NO:122), and the deduced translation product (SEQ ID NO:123).

20 Figure 60 shows a nucleic acid sequence of the mTRT cDNA.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention provides purified telomerase preparations and telomerase protein subunits useful for investigations of the activities of telomerases, including

25 potential nuclease activities. In particular, the present invention is directed to the telomerase and co-purifying polypeptides obtained from *Euplotes aediculatus*. This organism, a hypotrichous ciliate, was chosen for use in this invention as it contains an unusually large number of chromosomal ends (Prescott, Microbiol. Rev., 58:233 [1994]), because a very large number of gene-sized DNA molecules are present in its polyploid

30 macronucleus. *Tetrahymena*, a holotrichous ciliate commonly used in previous studies of

telomerase and telomeres, is as evolutionarily distant from *Euplotes* as plants are from mammals (Greenwood *et al.*, J. Mol. Evol., 3:163 [1991]).

The homology found between the 123 kDa *E. aediculatus* telomerase subunit and the L8543.12 sequence (SEQ ID NO:55) (*i.e.*, Est2 of *Saccharomyces cerevisiae*; See, 5 Lendvay *et al.*, Genetics 144:1399-1412 [1996]), *Schizosaccharomyces*, and human motifs, provided a strong basis for predicting that full human telomerase molecule would comprise a protein that is large, basic, and includes such reverse transcriptase motifs. Thus, the compositions and methods of the present invention are useful for the identification of other telomerases from a wide variety of species. The present invention describes the use of the 10 123 kDa reverse transcriptase motifs in a method to identify similar motifs in organisms that are distantly related to *Euplotes* (*e.g.*, *Oxytricha*), as well as organisms that are not related to *Euplotes* (*e.g.*, *Saccharomyces*, *Schizosaccharomyces*, mice, humans, etc.).

The present invention also provides additional methods for the study of the structure and function of distinct forms of telomerase. It is contemplated that the 15 telomerase proteins of the present invention will be useful in diagnostic applications, evolutionary (*e.g.*, phylogenetic) investigations, as well as development of compositions and methods for cancer therapy or anti-aging regimens. Although the telomerase protein subunits of the present invention themselves have utility, it further contemplated that the polypeptides of the present invention will be useful in conjunction with the RNA moiety 20 of the telomerase enzyme (*i.e.*, a complete telomerase).

It is also contemplated that methods and compositions of this invention will lead to the discovery of additional unique telomerase structures and/or functions. In addition, the present invention provides novel methods for purification of functional telomerase, as well as telomerase proteins. This affinity based method described in Example 3, is an 25 important aspect in the purification of functionally active telomerase, as are the two anti-TRT antibodies provided for by the invention. A key advantage of this procedure is the ability to use mild elution conditions, during which proteins that bind non-specifically to the column matrix are not eluted.

Telomerase is a ribonucleoprotein complex (RNP) comprising an RNA component 30 and a catalytic protein component. The present invention relates to the cloning and

characterization of the catalytic protein component of telomerase, referred to as "TRT" (telomerase reverse transcriptase). TRT is so named because this protein acts as an RNA-dependent DNA polymerase (reverse transcriptase), using the telomerase RNA component ("TR") to direct synthesis of telomere DNA repeat sequences. Moreover, TRT is evolutionarily related to other reverse transcriptases.

In one aspect, the present invention provides TRT genes and proteins from ciliates, fungi, and vertebrates, especially mammals, such as humans, human telomerase reverse transcriptase, referred to as "hTRT." TRT is of extraordinary interest and value because telomerase activity in human (and other mammalian cells) correlates with cell proliferative capacity, cell immortality, and the development of a neoplastic phenotype. For example, telomerase activity and levels of human TRT gene products are elevated in immortal human cells (such as malignant tumor cells and immortal cell lines) relative to mortal cells (such as most human somatic cells).

The present invention is, in one aspect, directed to the nucleic and amino acid sequences of the protein subunits of the *E. aediculatus* telomerase, as well as the nucleic and amino acid sequences of the telomerases from other organisms, including humans. In addition, the present invention is directed to the purification of functional telomerase. As described below the present invention also comprises various forms of telomerase, including recombinant telomerase and telomerase protein subunits, obtained from various organisms.

TRT was initially characterized following purification of telomerase from the ciliate *Euplotes aediculatus*. Extensive purification of *E. aediculatus* telomerase, using RNA-affinity chromatography and other methods, yielded the protein "p123". Surprisingly, p123 is unrelated to proteins previously believed to constitute the protein subunits of the telomerase holoenzyme (i.e., the p80 and p95 proteins of *Tetrahymena thermophila*). Analysis of the p123 DNA and protein sequences (Genbank Accession No. U95964; Figures 9 and 10) (SEQ ID NO:1 and SEQ ID NO:2) revealed reverse transcriptase (RT) motifs consistent with the role of p123 as the catalytic subunit of telomerase (see, e.g., Figures 17, 25, 55, 57). Moreover, p123 is related to a *S. cerevisiae* (yeast) protein, Est2p, which was known to play a role in maintenance of telomeres in *S.*

*cerevisiae* (Genbank Accession No. S5396), but not recognized as encoding a telomerase catalytic subunit protein (see, e.g., Lendvay et al., 1996, *Genetics*, 144:1399).

In one aspect, the present invention provides reagents and methods for identifying and cloning novel TRTs using: nucleic acid probes and primers generated or derived from the TRT polynucleotides disclosed herein (e.g., for cloning TRT genes and cDNAs);  
5 antibodies that specifically recognize the motifs or motif sequences or other TRT epitopes (e.g., for expression cloning TRT genes or purification of TRT proteins); by screening computer databases; or other means. For example, as described in Example 16, PCR (polymerase chain reaction) amplification of *S. pombe* DNA was carried out with  
10 degenerate-sequence primers designed from the *Euplotes* p123 RT motifs B' and C. Of four prominent products generated, one encoded a peptide sequence homologous to *Euplotes* p123 and *S. cerevisiae* Est2p. Using this PCR product as a probe, the complete sequence of the *S. pombe* TRT homologue was obtained by screening of *S. pombe* cDNA and genomic libraries and amplifying *S. pombe* RNA by reverse transcription and PCR  
15 (RT-PCR). The complete sequence of the *S. pombe* gene ("tez1" or "Sp\_Trt1p" or "trt1"; GenBank Accession No. AF015783; Figure 69, Figure 46) revealed that homology with p123 and Est2p was especially high in the reverse transcriptase motifs (see Figures 56, 58).

Amplification using degenerate primers derived from the telomerase RT motifs was also used to obtain TRT gene sequences in *Oxytricha trifallax* and *Tetrahymena thermophila*, as described in Examples 13 and 15, respectively.  
20

The *Euplotes* p123, *S. pombe* trt1, and *S. cerevisiae* Est2p sequences of the invention were used in a search of a computerized database of human expressed sequence tags (ESTs) using the program BLAST (Altschul et al, 1990, *J. Mol. Biol.* 215:403). Searching this database with the Est2p sequence did not indicate a match, but searching  
25 with p123 and trt1 sequences identified a human EST (Genbank accession no. AA281296) (SEQ ID NO:121), as described in Example 17, encoding a homologous protein. Complete sequencing of the cDNA clone containing the EST (hereinafter, "clone 712562"; see Figure 47, SEQ ID NO:122) showed that seven RT motifs were present. However, this clone could not encode a contiguous human TRT, because motifs B', C, D, and E were contained  
30 in a different ORF than the more NH<sub>2</sub>-terminal motifs. In addition, the distance between



motifs A and B' was substantially shorter than that of the three previously characterized TRTs.

A cDNA clone, pGRN121 (ATCC accession # 209016), encoding a functional hTRT (SEQ. ID. NO: 1) was isolated from a cDNA library derived from the human 293 cell line as described in Example 17. Comparing clone 712562 with pGRN121 showed that clone 712562 has a 182 base pair deletion between motifs A and B'. The additional 182 base pairs present in pGRN121 places all of the TRT motifs in a single open reading frame, and increases the spacing between the motif A and motif B' regions to a distance consistent with the other known TRTs. SEQ. ID. NO: 117 encodes a catalytically active telomerase protein having the sequence of SEQ ID NO: 118. The polypeptide of SEQ ID NO: 118 has 1132 residues and a calculated molecular weight of about 127 kilodaltons (kD).

TRT cDNAs possessing the 182 basepair deletion characteristic of the clone 712562 are detected following reverse transcription of RNA from telomerase-positive cells (e.g., testis and 293 cells). hTRT RNAs lacking this 182 base pair sequence are referred to generally as "182 variants" and may represent one, two, or several species. Although the hTRT variants lacking the 182 basepair sequence found in the pGRN121 cDNA (SEQ ID NO. 117) are unlikely to encode a fully active telomerase catalytic enzyme, they may play a role in telomerase regulation and/or have partial telomerase activity, such as telomere binding or hTR binding activity.

#### **The 123 kDa and 43 kDa Telomerase Subunit Protein Sequences of *Euplotes***

The nucleic acid and deduced amino acid sequences of the *Euplotes* 123 and 43 kDa protein subunits are shown in Figures 1-6. In accordance with the invention, any nucleic acid sequence which encodes *E. aediculatus* telomerase or its subunits can be used to generate recombinant molecules which express the *Euplotes* telomerase or its subunits.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of telomerase subunit protein sequences, some bearing minimal homology to the nucleotide sequences of any known and naturally occurring gene, may be produced. The invention contemplates each and every possible variation of

nucleotide sequence that could be made by selecting combinations based on possible codon choices, taking into account the use of the codon "UGA" as encoding cysteine in *E. aediculatus*. Other than the exception of the "UGA" codon, these combinations are made in accordance with the standard triplet genetic code as applied to the nucleotide sequence encoding naturally occurring *E. aediculatus* telomerase, and all such variations are to be considered as being specifically disclosed. For example, the amino acid sequences encoded by each of the three open reading frames of the 43 kDa nucleotide sequence are specifically included (SEQ ID NOS:4-6). It is contemplated that any variant forms of telomerase subunit protein be encompassed by the present invention, as long as the proteins are functional in assays such as those described in the Examples or elsewhere herein.

Although nucleotide sequences which encode *E. aediculatus* telomerase protein subunits and their variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring sequence under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding *E. aediculatus* telomerase protein subunits or their derivatives possessing a substantially different codon usage, including the "standard" codon usage employed by human and other systems. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic expression host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding telomerase subunits and their derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater or a shorter half-life, than transcripts produced from the naturally occurring sequence.

It is now possible to produce a DNA sequence, or portions thereof, encoding telomerase protein subunits and their derivatives entirely by synthetic chemistry, after which the synthetic gene may be inserted into any of the many available DNA vectors and cell systems using reagents that are well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding *E. aediculatus* protein

subunits or any portion thereof, as well as sequences encoding yeast or human telomerase proteins, subunits, or any portion thereof.

Also included within the scope of the present invention are polynucleotide sequences that are capable of hybridizing to the nucleotide sequence of any member of the telomerase genus, including the sequences of Figures 9 (DNA sequence of the gene encoding the 123 kDa telomerase protein subunit), 11 (DNA sequence of the gene encoding the 43 kDa telomerase protein subunit), 12 (open reading frames of the 43 kDa telomerase protein subunit), and 26 (DNA sequence of *S. cerevisiae* Est2), under various conditions of stringency. Thus, in one embodiment, the novel compositions of the invention, including TRT encoding nucleic acids and anti-TRT antibodies, can also be used to identify and purify a genus of TRTs, including TRT isoforms and telomerase or telomerase components from any other organisms.

One embodiment of the invention includes isoforms and homologues of the *Euploies* 43 kDa telomerase, including the human p43 homologue, which can also be identified and isolated using the unique reagents provided by the invention and the methods described herein.

In an additional embodiment, TRT and telomerase enzyme complex components are used to identify telomerase-associated components.

Hybridization conditions used to identify and isolate members of the TRT genus are based on the melting temperature ( $T_m$ ) of the nucleic acid binding complex or probe, as taught in Berger and Kimmel (Berger and Kimmel, *Guide to Molecular Cloning Techniques*, Meth. Enzymol., vol. 152, Academic Press, San Diego CA [1987]) incorporated herein by reference, and may be used at a defined "stringency".

Altered nucleic acid sequences encoding telomerase protein subunits which may be used in accordance with the invention include deletions, insertions or substitutions of different nucleotides resulting in a polynucleotide that encodes the same or a functionally equivalent telomerase subunit. The protein may also show deletions, insertions or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent telomerase subunit, or a subunit that lacks one or more TRT partial activities or has another peptide fused thereto. Deliberate amino acid substitutions may

be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the biological activity of the telomerase subunit is retained. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine, valine; glycine, alanine; asparagine, glutamine; serine, threonine; and phenylalanine, tyrosine.

Methods for DNA sequencing are well known in the art and employ such enzymes as the Klenow fragment of DNA polymerase I, Sequenase® (US Biochemical Corp, Cleveland OH), *Taq* DNA polymerase (Perkin Elmer, Norwalk CT), thermostable T7 polymerase (Amersham, Chicago IL), or combinations of recombinant polymerases and proofreading exonucleases such as the ELONGASE Amplification System marketed by Gibco BRL (Gaithersburg MD). Preferably, the process is automated with machines such as the Hamilton Micro Lab 2200 (Hamilton, Reno NV), Peltier Thermal Cycler (PTC200; MJ Research, Watertown MA) and the ABI 377 DNA sequencers (Perkin Elmer).

Also included within the scope of the present invention are alleles encoding human or other mammalian or other eukaryotic cell telomerase proteins and subunits. As used herein, the term "allele" or "allelic sequence" is an alternative form of the nucleic acid sequence encoding human telomerase proteins or subunits. Alleles result from mutations (*i.e.*, changes in the nucleic acid sequence), and generally produce altered mRNAs or polypeptides whose structure and/or function may or may not be altered. Any given gene may have no, one or many allelic forms. Common mutational changes that give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of amino acids. Each of these types of changes may occur alone, or in combination with the others, one or more times within a given sequence.

#### **Telomerase Reverse Transcriptase Genus and Characterizing Motifs**

The present invention provides isolated and/or recombinant genes and proteins having a sequence of a telomerase catalytic subunit protein (*i.e.*, telomerase reverse transcriptase) that typically are large, basic, proteins having *reverse transcriptase*

(RT) and *telomerase-specific* amino acid motifs. Because these motifs are conserved across diverse organisms, a genus of TRT genes from numerous organisms is provided by the invention and can be identified, isolated or synthesized using primers, nucleic acid probes, and antibodies of the invention, *i.e.*, such as those specific for one or more of the motif sequences.

The invention provides telomerase species of the genus of telomerase subunit proteins. The telomerase reverse transcriptase protein subunit is itself a member of the genus of reverse transcriptase proteins. The TRT species described herein illustrates structural features common to the members of the TRT genus in the form of structural motifs. These motifs can effect common telomerase functions. Sequence analysis of TRT species show that these species contain amino acid regions common to other reverse transcriptase (RT) proteins, as illustrated in Figures 17, 18, 25, 48, 55 and 57. This region is in the approximately the middle third of the hTRT mRNA (cDNA, SEQ ID NO:1); the most structurally conserved region of hTRT compared to reverse transcriptases from other organisms. Novel reagents of the invention corresponding to such motif regions can be used in methods of the invention to generate antibodies and nucleic acid probes and to identify additional isoforms and telomerase species from other organisms. The invention provides oligonucleotides corresponding to these motif regions, including the RT region, including restriction enzyme fragments and amplification products generated from a known telomerase. Oligonucleotides corresponding to motifs can also be synthesized *in vitro*. PCR primer pairs useful for amplifying RT motifs of TRT are described below. These oligonucleotide can also be used as PCR amplification primers or hybridization probes to identify and isolate additional human isoforms and telomerase species from other organisms. These oligonucleotides can also be used as primers to amplify additional TRT species, using techniques such as RACE, as described below.

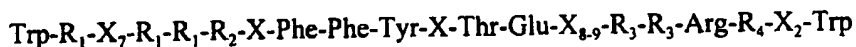
The seven RT motifs found in TRTs, while similar to those found in other reverse transcriptases, have particular hallmarks unique to the TRT genus. For example, as shown in Figure 55 and Figure 57C, within the TRT RT motifs there are a number of amino acid substitutions (marked with arrows) in residues highly conserved among the other RTs. For example, in motif C the two aspartic acid residues (DD) that coordinate

active site metal ions (see, Kohlstaedt et al., 1992, *Science* 256:1783; Jacobo-Molina et al., 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:6320; Patel et al., 1995, *Biochemistry* 34:5351) occur in the context hxDD(F/Y), more specifically, as (L/V)xDD(F/Y), in the telomerase RTs compared to (F/Y)xDDh in the other RTs (where h is a hydrophobic amino acid, and "x" is any amino acid; see Xiong et al., 1990, *EMBO J.* 9:3353; Eickbush, in *The Evolutionary Biology of Viruses*, (S. Morse, Ed., Raven Press, NY, p. 121, 1994).

Another systematic change characteristic of the telomerase subgroup occurs in motif E, where WxGxSx is a consensus sequence or is conserved among the telomerase proteins, whereas hLGxxh is characteristic of other RTs (see Figures 55 and 57C; Xiong (1990), *supra*; Eickbush (1994) *supra*). This motif E is called the "primer grip", and mutations in this region have been reported to affect RNA priming but not DNA priming (Powell et al., 1997, *J. Biol. Chem.* 272:13262). Figures 55 and 57C give sequence alignments of several telomerase RT primer grip regions (motif E), including hTRT. Because telomerase requires a DNA primer (*e.g.*, the chromosome 3' end) it is not unexpected that TRT should differ from other RTs in the primer grip region.

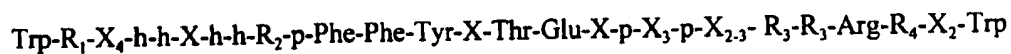
In addition, the distance between motifs A and B' is longer in the TRTs than is typical for other RTs, which may represent an insertion within the "fingers" region of the structure which resembles a right hand (See Figure 57B; see Kohlstaedt et al., *supra*; Jacobo-Molina et al., *supra*; and Patel et al., *supra*).

Moreover, as noted *supra*, the T motif is an additional hallmark of TRT proteins. The T motif, shown, *e.g.*, in Figure 55 and Figure 57A, comprises a sequence that can be described using the formula:



where X is any amino acid and the subscript refers to the number of consecutive residues, R<sub>1</sub> is leucine or isoleucine, R<sub>2</sub> is glutamine or arginine, R<sub>3</sub> is phenylalanine or tyrosine, and R<sub>4</sub> is lysine or histidine.

The T motif can also be described using the formula:



where X is any amino acid, a subscript refers to the number of consecutive residues, R<sub>1</sub> is leucine or isoleucine, R<sub>2</sub> is glutamine or arginine, R<sub>3</sub> is phenylalanine or tyrosine, R<sub>4</sub> is

lysine or histidine, h is a hydrophobic amino acid selected from Ala, Leu, Ile, Val, Pro, Phe, Trp, and Met, and p is a polar amino acid selected from Gly, Ser, Thr, Tyr, Cys, Asn and Gln.

In one embodiment, the present invention provides isolated naturally occurring and recombinant TRT proteins comprising one or more of the motifs illustrated in Figures 55 and 57, e.g.,

	Motif T	W-X <sub>12</sub> -FFY-X-TE-X <sub>10-11</sub> -R-X <sub>3</sub> -W-X <sub>7</sub> -I
	Motif T'	E-X <sub>2</sub> -V-X
	Motif 1	X <sub>3</sub> -R-X <sub>2</sub> -PK-X <sub>3</sub>
10	Motif 2	X-R-X-I-X
	Motif A	X <sub>4</sub> -F-X <sub>3</sub> -D-X <sub>4</sub> -YD-X <sub>2</sub>
	Motif B'	Y-X <sub>4</sub> -G-X <sub>2</sub> -QG-X <sub>3</sub> -S-X <sub>8</sub>
	Motif C	X <sub>6</sub> -DD-X-L-X <sub>3</sub>

When the TRT protein contains more than one TRT motif, the order (NH<sub>2</sub> -> COOH) is as shown in Figure 55.

In one embodiment, the present invention provides isolated naturally occurring TRT proteins comprising the following supermotif:

(NH<sub>2</sub>)-X<sub>300-600</sub>-W-X<sub>12</sub>-FFY-X-TE-X<sub>10-11</sub>-R-X<sub>3</sub>-W-X<sub>7</sub>-I-X<sub>5-20</sub>-E-X<sub>2</sub>-V-X-X<sub>5-20</sub>-X<sub>3</sub>-R-X<sub>2</sub>-PK-X<sub>4-10</sub>-R-X-I-X-X<sub>60-80</sub>-X<sub>4</sub>-F-X<sub>3</sub>-D-X<sub>4</sub>-YD-X<sub>2</sub>-X<sub>80-130</sub>-Y-X<sub>4</sub>-G-X<sub>2</sub>-QG-X<sub>3</sub>-S-X<sub>8</sub>-X<sub>5-35</sub>-X<sub>6</sub>-DD-X-L-X<sub>3</sub>-X<sub>10-20</sub>-X<sub>12</sub>-K

It will be apparent to one of skill that, provided with the reagents, and the TRT sequences disclosed herein for those reagents, and the methods and guidance provided herein (including specific methodologies described *infra*), TRT genes and proteins can be obtained, isolated and produced in recombinant form by one of ordinary skill. For example, primers (e.g., degenerate amplification primers) are provided that hybridize to gene sequences encoding RT and T motifs characteristic of TRT. One or more primers or degenerate primers that hybridize to sequences encoding the FFYXTE region of the T motif, other TRT motifs (as discussed *infra*), or combinations of motifs or consensus sequences, can be prepared based on the codon usage of the target organism, and

used to amplify the TRT gene sequence from genomic DNA or cDNA prepared from the target organism. Use of degenerate primers is well known in the art and entails sets of primers that hybridize to the set of nucleic acid sequences that can potentially encode the amino acids of the target motif, taking into account codon preferences and usage of the target organism, and by using amplification (e.g., PCR) conditions appropriate for allowing base mismatches in the annealing steps. Typically two primers are used; however, single primer (or, in this case, a single degenerate primer set) amplification systems are well known and may be used to obtain TRT genes.

Table 1 provides illustrative primers of the invention that may be used to amplify novel TRT nucleic acids, particularly those from vertebrates (e.g., mammals). "N" is an equimolar mixture of all four nucleotides and sequences within parentheses are equimolar mixtures of the specified nucleotides.

TABLE 1  
ILLUSTRATIVE DEGENERATE PRIMERS FOR AMPLIFICATION  
OF TRT NUCLEIC ACIDS

	<u>motif</u>	<u>direction</u>	<u>5'- sequence -3'</u>
20	a <u>FFYVTE</u>	Forward	TT(CT)TT(CT)TA(CT)GTNACNGA
	b <u>FFYVTE</u>	Reverse	TCNGTNAC(GA)TA(GA)AA(GA)AA
	c <u>RFIPKP</u>	Forward	(CA)GNTT(CT)AT(ACT)CCNAA(AG)CC
	d <u>RFIPKP</u>	Reverse	GG(TC)TTNGG(TGA)AT(GA)AANC
25	e <u>AYDTI</u>	Forward	GCNTA(CT)GA(CT)ACNAT
	f <u>AYDTI</u>	Reverse	TANGT(GA)TC(GA)TANGC
	g <u>GIPOG</u>	Forward	GGNAT(ACT)CCNCA(AG)GG
30	h <u>GIPOGS</u>	Reverse	(GC)(AT)NCC(TC)TGNGG(TGA)ATNCC
	i <u>LVDDFL</u>	Forward	(CT)TNGTNGA(CT)GA(CT)TT(CT)(CT)T
	j <u>DDFLVLT</u>	Reverse	GTNACNA(GA)NA(GA)(GA)AA(GA)TC(GA)TC



(TABLE 1:continued)

Allowed primer combinations (y = yes, n = no)

		<u>Reverse</u>				
		<u>Forward</u>	<u>b</u>	<u>d</u>	<u>f</u>	<u>h</u> <u>i</u>
5	a -		n	y	y	y y
	c -		n	n	y	y y
	e -		n	n	n	y y
	g -		n	n	n	n y
	i -		n	n	n	n n

10

In one embodiment, an amplified TRT nucleic acid is used as a hybridization probe for colony hybridization to a library (e.g., cDNA library) made from the target organism, such that a nucleic acid having the entire TRT protein coding sequence, or a substantial portion thereof, is identified and isolated or cloned. In this manner, the invention provides the methods and reagents to identify, isolate and clone all species of the TRT genus. As illustrative examples, reagents and methods such as those just described were used in accordance with the methods described herein to obtain many species of the TRT genus of gene sequences, including human, mouse, *Euplotes aediculatus* 123 kDa and 43 kDa species, *S. cerevisiae*, *Schizosaccharomyces pombe*, *Oxytricha trifallax* and *Tetrahymena thermophila*. It will be recognized that following cloning of a previously uncharacterized TRT specie gene, the sequence can be determined by routine methods and the encoded polypeptide synthesized and assayed for a TRT activity, such as telomerase catalytic activity (as described herein and/or by telomerase assays known in the art).

25

It will also be apparent to those of skill that all TRT genes and polypeptides are within the scope of the claimed genus because they can be cloned using the unique reagents provided for by the invention and can be identified, isolated and cloned using any of a variety of cloning methods. Use of the TRT motif-containing nucleic acids and polypeptides of the invention can be used in a wide variety of such methods. For example, hybridization using a probe based on the sequence of a known TRT to DNA or other nucleic acid libraries from the target organism can be used as described in the Examples below. It will be appreciated that degenerate PCR primers

30

or their amplification products may themselves be labeled and used as hybridization probes. In another embodiment, expression cloning methods are used.

In a further embodiment, the peptides and proteins provided for by the invention can be produced by synthetic or by recombinant means to generate  
5 antibodies, that in turn can react specifically with a TRT from any species, such as human TRTs, including, for example, hTRT isoforms and human p43 homologues. For example, one or more antibodies that specifically bind peptides that span a TRT motif or other TRT epitope, such as the FFYXTE motif (where X is any of the twenty standard amino acids) can be employed to isolate a ribosomal complex comprising a  
10 TRT protein and the mRNA that encodes it.

For generating such antibodies of the invention, the peptide immunogens are typically between 6 and 30 amino acids in length, more often about 10 to 20 amino acids in length. The antibodies may also be used to probe a cDNA expression library derived from the organism of interest to identify a clone encoding a TRT sequence.  
15 another embodiment, computer searches of DNA databases for DNAs containing sequences conserved with known TRTs can also be used to identify a clone encoding a TRT sequence.

### Human Telomerase Motifs

20 The present invention also provides nucleic and amino acid sequence information for human telomerase motifs. These sequences were first identified in a BLAST search conducted using the *Euplotes* 123 kDa peptide, and a homologous sequence from *Schizosaccharomyces pombe*, designated as "tez1" (SEQ ID NO:69).

Figure 25 shows the sequence alignment of the *Euplotes* ("p123")(SEQ ID  
25 NO:65); *Schizosaccharomyces* ("tez1") (SEQ ID NO:63); yeast Est2p (SEQ ID NO:64) (*i.e.*, the *S. cerevisiae* protein encoded by the *Est2* nucleic acid sequence (SEQ ID NO:55), and also referred to herein as "L8543.12"); and the human homolog (SEQ ID NO:61) identified in this comparison search. The human amino acid sequence of this aligned portion is SEQ ID NOS:61 and 67 (Figures 25 and 27) (the corresponding  
30 cDNA coding sequence is provided in SEQ ID NO:62, Figure 28). The portion of tez1

shown in Figure 25 is SEQ ID NO:63, the portion of yeast Est2 shown is SEQ ID NO:64, and the portion of *Euplotes* p123 shown is SEQ ID NO:65.

As shown in Figure 25, there are regions that are highly conserved among these proteins. For example, as shown in this Figure, there are regions of identity in "Motif 0," "Motif 1," "Motif 2," and "Motif 3." The identical amino acids are indicated with an asterisk (\*), while the similar amino acid residues are indicated by a circle (M). This indicates that there are regions within the telomerase motifs that are conserved among a wide variety of eukaryotes, ranging from yeast to ciliates, to humans. It is contemplated that additional organisms will likewise contain such conserved regions of sequence.

Figure 27 shows the amino acid sequence (SEQ ID NO:67, see also Figure 25, SEQ ID NO:61) of a cDNA clone encoding human telomerase motifs. Figure 28 shows the DNA sequence encoding the amino acid sequence of Figure 27 (SEQ ID NO:62), which includes human telomerase peptide motifs. This human amino acid sequence as aligned with other TRT species is provided in SEQ ID NO:61, Figure 25. Figure 29 shows the amino acid sequence of *S. pombe* *tez1* (SEQ ID NO:68), while Figure 30 shows the DNA sequence of *tez1* (SEQ ID NO:69). In Figure 30, the introns and other non-coding regions are shown in lower case, while the exons (*i.e.*, coding regions are shown in upper case.

The present invention provides oligonucleotide primers and probes that can hybridize specifically to nucleic acids having the TRT protein-encoding or cDNA nucleic acid sequence (*i.e.*, SEQ ID NO:117) or encoding the protein sequence of a TRT (*i.e.*, SEQ ID NO:118) and such reagents can be used to identify and amplify a wide variety of species of the genus of telomerase protein-encoding sequences. Intronic and genomic (non-transcribed) sequences can also be amplified using the PCR primers of the invention to identify new TRT species. For illustrative purposes, PCR primers and amplification methods are described.

Amplification of TRT sequences which are conserved among the different members of the genus, *i.e.*, consensus TRT sequences, such as TRT and RT motifs, can be used to generate oligonucleotide reagents of the invention for use as hybridization

probes to identify and isolate additional isoforms and TRT species from other organisms. These oligonucleotides can also be used as primers to amplify additional TRT species or sequences, using techniques such as RACE, as described below.

Oligonucleotides can be used to identify and detect additional telomerase species using a variety of hybridization techniques and conditions. One of skill in the art will appreciate that, whatever amplification or hybridization method is used, if a quantitative result is desired, care must be taken to use a method that maintains or controls for the relative frequencies of the amplified or other target nucleic acids. Suitable amplification methods include, but are not limited to: polymerase chain reaction, PCR (PCR PROTOCOLS, A GUIDE TO METHODS AND APPLICATIONS, *ed.* Innis, Academic Press, N.Y. (1990) and PCR STRATEGIES (1995), *ed.* Innis, Academic Press, Inc., N.Y. (Innis )), ligase chain reaction (LCR). (Wu (1989) *Genomics* 4:560; Landegren (1988) *Science* 241:1077; Barringer (1990) *Gene* 89:117); transcription amplification (Kwoh *Proc. Natl. Acad. Sci. USA*, 86:1173 (1989)); self-sustained sequence replication (Guatelli (1990) *Proc. Natl. Acad. Sci. USA*, 87:1874); Q Beta replicase amplification and other RNA polymerase mediated techniques (*e.g.*, NASBA, Cangene, Mississauga, Ontario); see Berger (1987) *Methods Enzymol.* 152:307-316, Sambrook, and Ausubel, as well as Mullis (1987) U.S. Patent Nos. 4,683,195 and 4,683,202; Arnheim (1990) *C&EN* 36-47; Lomell *J. Clin. Chem.*, 35:1826 (1989); Van Brunt, *Biotechnology*, 8:291-294 (1990); Wu (1989) *Gene* 4:560; Sooknanan (1995) *Biotechnology* 13:563-564. Methods for cloning *in vitro* amplified nucleic acids are described in Wallace, U.S. Pat. No. 5,426,039.

The invention provides for amplification and manipulation or detection of the products from each of the above methods to prepare DNA encoding TRT protein. In PCR techniques, oligonucleotide primers complementary to the two borders of the DNA region to be amplified are synthesized and used (see, Innis). PCR can be used in a variety of protocols to amplify, identify, isolate and manipulate nucleic acids encoding human telomerase. In these protocols, standard methods for selecting appropriate primers and probes are described. The present invention provides primers and probes for identifying and amplifying DNA encoding human telomerase protein

and can be generated to comprise all or a portion of any of the nucleic acid sequences listed herein.

PCR-amplified sequences can also be labeled and used as detectable oligonucleotide probes, but such nucleic acid probes can be generated using any  
5 synthetic or other technique well known in the art, as described above. The labeled amplified DNA or other oligonucleotide or nucleic acid of the invention can be used as probes to further identify and isolate TRT protein species or isoforms from various cDNA or genomic libraries.

The present invention provides RACE-based methods for isolating TRT nucleic  
10 acids from any organism (RACE is another PCR-based approach for DNA amplification). Briefly, this technique involves using PCR to amplify a DNA sequence using a random 5' primer and a defined 3' primer (5' RACE) or a random 3' primer and a defined 5' primer (3' RACE). The amplified sequence is then subcloned into a vector where can be sequenced and manipulated using standard techniques. The RACE  
15 method is well known to those of skill in the art and kits to perform RACE are commercially available (*e.g.* Gibco BRL #18374-058 (5' RACE) or #18373-019 (3' RACE)(Gaithersburg, MD)), see also Lankiewicz (1997) *Nucleic Acids Res* 25:2037-2038; Frohman (1988) *Proc. Natl. Acad. Sci. USA* 85:8998.

For 5' RACE, a primer, the gene-specific primer, is selected near the 5' end of  
20 the known sequence oriented to extend towards the 5' end. The primer is used in a primer extension reaction using a reverse transcriptase and mRNA. After the RNA is optionally removed, the specifically-primed cDNA is either: 1) "tailed" with deoxynucleotide triphosphates (dNTP) and dideoxyterminal transferase, then a primer that is complementary to the tail with a 5' end that provides a unique PCR site and the  
25 first gene-specific primer is used to PCR amplify the cDNA; or, 2) an oligonucleotide that provides a unique PCR site is ligated to an end of the cDNA using RNA ligase; then a primer complementary to the added site and the first gene-specific primer is used to PCR amplify the cDNA. Subsequent amplifications are usually performed with a gene-specific primer nested with respect to the first primer. Amplified products are

then purified, usually by gel electrophoresis, then sequenced and examined to see if they contain the additional cDNA sequences desired.

For 3' RACE, an oligo dT-primer is annealed to the poly-A tails of an mRNA and then extended by a reverse transcriptase. Usually the oligo dT primer has a 5' end that provides a unique PCR site. The RNA is then removed, optionally, or dissociated, and the cDNA is amplified with a primer to the oligo dT tail and a gene-specific primer near the 3' end of the known sequence (oriented towards the 3' end). Subsequent amplifications are performed and amplified products purified, as described for 5' RACE.

Another useful means of obtaining nucleic acids of the invention, such as large genomic clones, is to screen BAC or P1 genomic libraries. BACs, bacterial artificial chromosomes, are vectors that can contain 120+ Kb inserts. BACs are based on the *E. coli* F factor plasmid system and are simple to manipulate and purify in microgram quantities. Because BAC plasmids are kept at one to two copies per cell, the problems of rearrangement observed with YACs, which can also be employed in the present methods, are eliminated. BAC vectors can include marker genes for luciferase and green fluorescent protein (GFP) (Baker (1997) *Nucleic Acids Res* 25:1950-1956). P1 is a bacteriophage that infects *E. coli* that can contain 75-100 Kb DNA inserts (Mejia (1997) *Genome Res* 7:179-186; Ioannou (1994) *Nat Genet* 6:84-89), and screened in much the same way as lambda libraries.

The polynucleotide sequence encoding telomerase, or telomerase protein subunits, or their functional equivalents, may be extended utilizing partial nucleotide sequence and various methods known in the art to detect upstream sequences such as promoters and regulatory elements. For example, Gobinda (1993) *PCR Meth. Applic.* 2:318-22, describes "restriction-site" polymerase chain reaction (PCR) as a direct method which uses universal primers to retrieve unknown sequence adjacent to a known locus. First, genomic DNA is amplified in the presence of primer to a linker sequence and a primer specific to the known region. The amplified sequences are subjected to a second round of PCR with the same linker primer and another specific

primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR can be used to amplify or extend sequences using divergent primers based on a known region (Triglia *et al.*, Nucleic Acids Res 16:8186 [1988]).

5 The primers may be designed using OLIGO® 4.06 Primer Analysis Software (National Biosciences Inc, Plymouth MN [1992]), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68E-72EC. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment  
10 is then circularized by intramolecular ligation and used as a PCR template.

Capture PCR (Lagerstrom *et al.* PCR Methods Applic 1:111-19 [1991]), a method for PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA, may also be used. Capture PCR also requires multiple restriction enzyme digestions and ligations to place an engineered  
15 double-stranded sequence into an unknown portion of the DNA molecule before PCR.

Another method which may be used to retrieve unknown sequence is walking PCR (Parker *et al.*, Nucleic Acids Res 19:3055-60 [1991]), a method for targeted gene walking. Alternatively, PCR, nested primers, PromoterFinder™ (Clontech, Palo Alto CA) and PromoterFinder libraries can be used to walk in genomic DNA. This process  
20 avoids the need to screen libraries and is useful in finding intron/exon junctions.

Preferred libraries for screening for full length cDNAs are ones that have been size-selected to include larger cDNAs. Also, random primed libraries are preferred in that they will contain more sequences which contain the 5' and upstream regions of genes. A randomly primed library may be particularly useful if an oligo d(T) library  
25 does not yield a full-length cDNA. Genomic libraries are useful for extension into the 5' nontranslated regulatory region.

Capillary electrophoresis may be used to analyze either the size or confirm the nucleotide sequence in sequencing or PCR products. Systems for rapid sequencing are available from Perkin Elmer, Beckman Instruments (Fullerton CA), and other  
30 companies. Capillary sequencing may employ flowable polymers for electrophoretic

separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity is converted to electrical signal using appropriate software (*e.g.*, Genotyper™ and Sequence Navigator™ from Perkin Elmer) and the entire process  
5 from loading of samples to computer analysis and electronic data display is computer controlled. Capillary electrophoresis is particularly suited to the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample. The reproducible sequencing of up to 350 bp of M13 phage DNA in 30 min has been reported (Ruiz-Martinez *et al.*, Anal Chem 65:2851-8 [1993]).

10

### Expression of the Nucleotide Sequence

In accordance with the present invention, polynucleotide sequences which encode telomerase, telomerase protein subunits, or their functional equivalents, may be used in recombinant DNA molecules that direct the expression of telomerase or  
15 telomerase subunits by appropriate host cells.

The nucleotide sequences of the present invention can be engineered in order to alter either or both telomerase subunits for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression and/or activity of the gene product. For example, mutations may be introduced using  
20 techniques which are well known in the art (*e.g.*, site-directed mutagenesis to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to produce splice variants, to alter activity, etc.).

### Expression Systems

25 In order to express a biologically active telomerase protein subunit, the nucleotide sequence encoding the subunit or the functional equivalent, is inserted into an appropriate expression vector (*i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence). In order to express a biologically active telomerase enzyme, the nucleotide sequence encoding the  
30 telomerase protein subunits are inserted into appropriate expression vectors and the



nucleotide sequence encoding the telomerase RNA subunit is inserted into the same or another vector for RNA expression. The protein and RNA subunits are then either expressed in the same cell or expressed separately, and then mixed to achieve a reconstituted telomerase.

5           Methods which are well known to those skilled in the art can be used to construct expression vectors containing a telomerase protein subunit sequence and appropriate transcriptional or translational controls. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination or genetic recombination. Such techniques are described in Sambrook *et al.* (Sambrook *et*  
10 *al.*, *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Plainview NY [1989]), and Ausubel *et al.* (Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, New York NY [1989]). These same methods may be used to convert the UGA codons, which encode cysteine in *Euplotes*, to the UGU or UGC codon for cysteine recognized by the host expression system.

15           A variety of expression vector/host systems may be utilized to contain and express a telomerase subunit-encoding sequence. These include but are not limited to microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell  
20 systems transfected with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmid); or animal cell systems.

          The "control elements" or "regulatory sequences" of these systems vary in their strength and specificities and are those non-translated regions of the vector, enhancers,  
25 promoters, and 3' untranslated regions, which interact with host cellular proteins to carry out transcription and translation. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in  
bacterial systems, inducible promoters such as the hybrid *lacZ* promoter of the  
30 Bluescript® phagemid (Stratagene, La Jolla CA) or pSport1 (Gibco BRL) and *ptrp-lac*

hybrids and the like may be used. The baculovirus polyhedron promoter may be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (e.g., heat shock, RUBISCO; and storage protein genes) or from plant viruses (e.g., viral promoters or leader sequences) may be cloned into the vector. In mammalian cell systems, promoters from the mammalian genes or from mammalian viruses are most appropriate. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding telomerase or telomerase protein subunits, vectors based on SV40 or EBV may be used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the telomerase protein or subunit. For example, when large quantities of telomerase protein, subunit, or peptides, are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be desirable. Such vectors include, but are not limited to, the multi functional *E. coli* cloning and expression vectors such as Bluescript® (Stratagene), in which the sequence encoding the telomerase or protein subunit may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of beta-galactosidase so that a hybrid protein is produced (e.g., pin vectors; Van Heeke and Schuster, J. Biol. Chem., 264:5503-5509 [1989]) and the like. pGEX vectors (Promega, Madison WI) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems are designed to include heparin, thrombin or factor Xa protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase and PGH may be used. For reviews, see Ausubel *et al.* (*supra*) and Grant *et al.*, Meth. Enzymol., 153:516-544 (1987).

In cases where plant expression vectors are used, the expression of a sequence encoding telomerase or a telomerase protein subunit, can be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV (Brisson *et al.*, Nature 310:511-514 [1984]) can be used alone or in combination  
5 with the omega leader sequence from TMV (Takamatsu *et al.*, EMBO J., 6:307-311 [1987]). Alternatively, plant promoters such as the small subunit of RUBISCO (Coruzzi *et al.* EMBO J., 3:1671-1680 [1984]; Broglie *et al.*, Science 224:838-843 [1984]) or heat shock promoters (Winter and Sinibaldi Results Probl. Cell Differ., 17:85-105 [1991]) can be used. These constructs can be introduced into plant cells by  
10 direct DNA transformation or pathogen-mediated transfection (for reviews of such techniques, see Hobbs or Murry, in *McGraw Hill Yearbook of Science and Technology* McGraw Hill New York NY, pp. 191-196 [1992]; or Weissbach and Weissbach, *Methods for Plant Molecular Biology*, Academic Press, New York NY, pp. 421-463 [1988]).

15 An alternative expression system which can be used to express telomerase or telomerase protein subunit is an insect system. In one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequence encoding the telomerase subunit of interest can be cloned into a nonessential region of the virus,  
20 such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the sequence encoding the telomerase protein or telomerase protein subunit will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses are then used to infect *S. frugiperda* cells or *Trichoplusia* larvae in which the telomerase subunit sequence is expressed  
25 (Smith *et al.*, J. Virol., 46:584 [1983]; Engelhard *et al.*, Proc. Natl. Acad. Sci. 91:3224-7 [1994]).

In mammalian host cells, a number of viral-based expression systems can be utilized. In cases where an adenovirus is used as an expression vector, a sequence encoding a telomerase protein or telomerase protein subunit, can be ligated into an  
30 adenovirus transcription/ translation complex consisting of the late promoter and

tripartite leader sequence. Insertion in a nonessential E1 or E3 region of the viral genome will result in a viable virus capable of expressing in infected host cells (Logan and Shenk, Proc. Natl. Acad. Sci., 81:3655-59 [1984]). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase  
5 expression in mammalian host cells.

Specific initiation signals may also be required for efficient translation of a sequence encoding telomerase protein subunits. These signals include the ATG initiation codon and adjacent sequences. In cases where the sequence encoding a telomerase protein subunit will be expressed by the host cell, its initiation codon and  
10 upstream sequences can be inserted into the most appropriate expression vector, and no additional translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, or the cell's regulatory environment will inhibit transcription, exogenous transcriptional control signals including the ATG initiation codon can be provided. The initiation codon should be in the correct reading  
15 frame to ensure transcription of the entire insert. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate to the cell system in use (Scharf *et al.*, Results Probl. Cell Differ., 20:125 [1994]; and Bittner *et al.*, Meth. Enzymol., 153:516 [1987]).

20 In addition, a host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be  
25 important for correct insertion, folding and/or function. Different host cells such as CHO (ATCC CCL 61 and CRL 9618), HeLa (ATCC CCL 2), MDCK (ATCC CCL 34 and CRL 6253), HEK 293 (ATCC CRL 1573), WI-38 (ATCC CCL 75) (ATCC: American Type Culture Collection, Rockville, MD) have specific cellular machinery and characteristic mechanisms for such post-translational activities and can be chosen

to ensure the correct modification and processing of the introduced, recombinant protein.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express telomerase or a telomerase subunit protein may be transformed using expression vectors which contain viral origins of replication or endogenous expression elements and a selectable marker gene. Following the introduction of the vector, cells may be allowed to grow for 1-2 or more days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clumps of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler *et al.*, Cell 11:223-32 [1977]) and adenine phosphoribosyltransferase (Lowy *et al.*, Cell 22:817 [1980]) genes which can be employed in tk- or apt- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, *dhfr* confers resistance to methotrexate (Wigler *et al.*, Proc. Natl. Acad. Sci., 77:3567 [1980]); *npt*, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin *et al.*, J. Mol. Biol., 150:1 [1981]) and *als* or *pat*, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *In McGraw Hill Yearbook of Science and Technology*, McGraw Hill, New York NY, pp 191-196, [1992]). Additional selectable genes have been described, for example, *trpB*, which allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman and Mulligan, Proc. Natl. Acad. Sci., 85:8047 [1988]). Recently, the use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate, GUS, and luciferase and its substrate, luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression

attributable to a specific vector system (Rhodes *et al.*, Meth. Mol. Biol., 55:121 [1995]).

### Nucleic Acid Hybridization Techniques

The hybridization techniques disclosed herein can be utilized to identify, isolate  
5 and characterize genes and gene products (*i.e.*, mRNA) encoding the TRT proteins of  
the invention, including TRTs from different species and allelic variations of TRT in a  
specie. A variety of methods for specific DNA and RNA detection and measurement  
using nucleic acid hybridization techniques are known to those of skill in the art. *See*  
NUCLEIC ACID HYBRIDIZATION, A PRACTICAL APPROACH, Ed. Hames, B.D. and  
10 Higgins, S.J., IRL Press, 1985; Gall (1989) *Proc. Natl. Acad. Sci.*, U.S.A. 63:378; and  
Sambrook. Depending on an application, the selection of a DNA hybridization format  
is often optional. For example, one method for evaluating the presence or absence of  
DNA encoding a telomerase protein in a sample involves a Southern transfer. Briefly,  
the nucleic acid sample, such as digested DNA or mRNA, is run on agarose slab or  
15 polyacrylamide gels in buffer and transferred to membranes. Hybridization is carried  
out using nucleic acid probes. For the TRT nucleic acids of this invention, the nucleic  
acid probes may comprise nucleic acid sequences conserved amongst the genus of TRT  
nucleic acids. Preferably nucleic acid probes are 10 to 20 to 30 or more bases or longer  
in length (see Sambrook for methods of selecting nucleic acid probe sequences for use  
20 in nucleic acid hybridization). Both quantitative and qualitative determination of the  
presence or absence of DNA or RNA encoding TRT protein can be performed in  
accordance with the present methods.

Similarly, and as but one of many examples, a Northern transfer can be used for  
the detection of mRNA encoding telomerase protein. For example, mRNA is isolated  
25 from a given cell sample using an acid guanidinium-phenol-chloroform extraction  
method. The mRNA is then electrophoresed to separate the mRNA species and the  
mRNA is transferred from the gel to a nitrocellulose membrane. As with the Southern  
transfers, probes, such as labeled probes or PCR amplification products can be used to  
identify the presence or absence of telomerase protein-encoding nucleic acid. The  
30 hTRT mRNA of the invention is often expressed in cells at such low levels that it can

be extremely difficult to detect by Northern blotting, even using the most sensitive assays. This can be true even with cells that express relatively high levels of hTRT mRNA, such as immortal and cancer cells. Because of the typically very low level of expression of telomerase mRNA, an optimized Northern blot protocol is described  
5 below.

The low level of telomerase mRNA, even in TRT-positive cells, *i.e.*, cells that express telomerase activity, such as cancer cells, is reflected by the low levels of TRT protein that may be seen in such cells. Such protein can be detected by the detection methods of the invention, including immunoblotting (Western blots). TRT protein in  
10 the human cancer cell line 293 can be detected using a sensitive Western blot system employing anti-telomerase polyclonal antisera of the invention, although the TRT signal on the Western blot was weak, in part showing that hTRT is present in low or very low abundance even in immortal cells.

Sandwich assays are commercially useful hybridization assays for detecting or  
15 isolating protein or nucleic acid. Such assays utilize a "capture" nucleic acid or protein that is often covalently immobilized to a solid support and a labeled "signal" nucleic acid, typically in solution. A clinical or other sample provides the target nucleic acid or protein. The "capture" nucleic acid or protein and "signal" nucleic acid or protein hybridize with or bind to the target nucleic acid or protein to form a "sandwich"  
20 hybridization complex. To be effective, the signal nucleic acid or protein cannot hybridize or bind substantially with the capture nucleic acid or protein.

Typically, oligonucleotide probes are labeled signal nucleic acids that are used to detect hybridization. Complementary probe nucleic acids or signal nucleic acids may be labeled for use in any one of several methods typically used to detect the  
25 presence of hybridized polynucleotides. Methods of detection can use labels for autoradiography or autofluorography, such as  $^3\text{H}$ ,  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^{32}\text{P}$ -labeled probes or the like (see definition of label, above). Other labels include ligands which bind to labeled antibodies, fluorophores, chemiluminescent agents, enzymes, and antibodies which can serve as specific binding pair members for a labeled ligand.

Detection of a hybridization complex may require the binding of a signal generating complex to a duplex of target and probe polynucleotides or nucleic acids. Typically, such binding occurs through ligand and anti-ligand interactions as between a ligand-conjugated probe and an anti-ligand conjugated with a signal, i.e., antibody-antigen or complementary nucleic acid binding. The label may also allow indirect detection of the hybridization complex. For example, where the label is a hapten or antigen, the sample can be detected by using antibodies. In these systems, a signal is generated by attaching fluorescent or enzymatic molecules to the antibodies or, in some cases, by attachment of a radioactive label. The sensitivity of the hybridization assays may be enhanced through use of a target nucleic acid or signal amplification system which multiplies the target nucleic acid or signal being detected. *In vitro* amplification techniques suitable for amplifying sequences for use as molecular probes or for generating nucleic acid fragments for subsequent subcloning are known, as described above. These systems can be used to directly identify allelic variations or mutated sequences where the PCR or LCR primers or other reagents are designed to be extended or ligated only when a specific sequence is present. Alternatively, the specific sequences can be generally amplified using, for example, more generic PCR primers and the amplified target region later probed or sequenced to identify a specific sequence indicative of the allele or mutation.

It will be appreciated that nucleic acid hybridization assays can also be performed in an array-based format. Arrays are a multiplicity of different "probe" or "target" nucleic acids (or other compounds) are hybridized against a target nucleic acid. In this manner a large number of different hybridization reactions can be run essentially "in parallel". This provides rapid, essentially simultaneous, evaluation of a wide number of reactants. Methods of performing hybridization reactions in array based formats are well known to those of skill in the art, e.g., Jackson (1996) *Nature Biotechnology* 14:1685; Chee, *Science* 274:610 (1995).

An alternative means for determining the level of expression of a gene encoding a protein is *in situ* hybridization. *In situ* hybridization assays are well known and are generally described in Angerer (1987) *Methods Enzymol* 152:649. In an *in situ*



hybridization assay, cells are fixed to a solid support, typically a glass slide or analyzed by a fluorescence activated cell sorter (FACS). If DNA is to be probed, the cells are typically denatured with heat or alkali. The cells are then contacted with a hybridization solution at a moderate temperature to permit annealing of labeled probes  
5 specific to the nucleic acid sequence encoding the protein. The probes are typically labeled, *i.e.*, with radioisotopes or fluorescent reporters. See also U.S. Patent No. 5,583,016, and USSNs 08/770,564 and 08/770,565, both filed 20 December 1996; Soder (1997) *Oncogene* 14:1013-1021, which describe, *e.g.*, *in situ* hybridization of hTR. Another well-known *in situ* hybridization technique is the so-called FISH  
10 fluorescence *in situ* hybridization, as described by Macechko (1997) *J Histochem Cytochem* 45:359-363; and, Raap (1995) *Hum Mol Genet* 4(4), 529-534.

#### Identification of Transformants Containing the Polynucleotide Sequence

Although the presence/absence of marker gene expression suggests that the gene  
15 of interest is also present, its presence and expression can be confirmed. For example, if the sequence encoding a telomerase protein subunit is inserted within a marker gene sequence, recombinant cells containing the sequence encoding the telomerase protein subunit can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with the sequence encoding telomerase protein  
20 subunit under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem sequence as well.

Alternatively, host cells which contain the coding sequence for telomerase or a telomerase protein subunit and express the telomerase or protein subunit be identified  
25 by a variety of standard procedures known to those of skill in the art using methods and reagents of the invention. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridization and protein bioassay or immunoassay techniques which include membrane, solution, or chip-based technologies for the detection and/or quantification of the nucleic acid or protein.

The presence of the polynucleotide sequence encoding telomerase protein subunits can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes, portions, or fragments of the sequence encoding the subunit. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on the nucleic acid sequence to detect transformants containing DNA or RNA encoding the telomerase subunit. As used herein "oligonucleotides" or "oligomers" refer to a nucleic acid sequence of approximately 10 nucleotides or greater and as many as approximately 100 nucleotides, preferably between 15 to 30 nucleotides, and more preferably between 20-25 nucleotides which can be used as a probe or amplimer.

A variety of standard protocols for detecting and measuring the expression of proteins using either polyclonal or monoclonal antibodies specific for the protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and fluorescent activated cell sorting (FACS). These and other assays are described, among other places, in Hampton *et al.*, *Serological Methods a Laboratory Manual*, APS Press, St Paul MN [1990]) and Maddox *et al.*, *J. Exp. Med.*, 158:1211 [1983]).

A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting related sequences include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide or primer. Alternatively, a telomerase protein subunit sequence, or any portion of it, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3 or SP6 and labeled nucleotides.

A number of companies such as Pharmacia Biotech (Piscataway NJ), Promega (Madison WI), and US Biochemical Corp (Cleveland OH) supply commercial kits and protocols for these procedures. Suitable reporter molecules or labels include those radio nuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles and the like. Patents teaching the

use of such labels include U.S. Patents 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241, herein incorporated by reference. Also, recombinant immunoglobulins may be produced as shown in U.S. Patent No. 4,816,567 incorporated herein by reference.

5

### **Purification of Telomerase and Telomerase Subunit Proteins**

In addition to the illustrative method of purification of a TRT species described in Example 3 below, it is contemplated that additional methods of purifying (recovering) TRT from naturally sources or recombinantly produced telomerase or telomerase protein subunits will be used in accordance with the methods of the invention. Examples of methods for purifying telomerase and compositions used in the methods of the invention are described below.

#### *Solubility Fractionation*

If the protein mixture is complex, an initial salt fractionation can separate many of the unwanted host cell proteins (or proteins derived from the cell culture media) from the recombinant protein of interest. The preferred salt is ammonium sulfate. Ammonium sulfate precipitates proteins by effectively reducing the amount of water in the protein mixture. Proteins then precipitate on the basis of their solubility. The more hydrophobic a protein is, the more likely it is to precipitate at lower ammonium sulfate concentrations. A typical protocol is to add saturated ammonium sulfate to a protein solution so that the resultant ammonium sulfate concentration is between 20-30%. This will precipitate the most hydrophobic of proteins. The precipitate is discarded (unless the protein of interest is hydrophobic) and ammonium sulfate is added to the supernatant to a concentration known to precipitate the protein of interest. The precipitate is then solubilized in buffer and the excess salt removed if necessary, either through dialysis or diafiltration. Other methods that rely on solubility of proteins, such as cold ethanol precipitation, are well known to those of skill in the art and can be used to fractionate complex protein mixtures.

### *Size Differential Filtration*

If the size of the protein of interest is known or can be estimated from the cDNA sequence, as is the case with the genus of TRT proteins and the illustrative species herein, proteins of greater and lesser size can be removed by ultrafiltration through  
5 membranes of different pore size (for example, Amicon or Millipore membranes). As a first step, the protein mixture is ultrafiltered through a membrane with a pore size that has a lower molecular weight cut-off than the molecular weight of the protein of interest. The retentate of the ultrafiltration is then ultrafiltered against a membrane with  
10 a molecular cut off greater than the molecular weight of the protein of interest. The recombinant protein will pass through the membrane into the filtrate. The filtrate can then be chromatographed.

### *Column Chromatography*

Proteins can be separated on the basis of their size, net surface charge, hydrophobicity and affinity for ligands. In addition, antibodies raised against proteins  
15 can be conjugated to column matrices and the proteins immunopurified. All of these general methods are well known in the art. See Scopes, R. K., Protein Purification: Principles and Practice, 2nd ed., Springer Verlag, (1987). Chromatographic techniques can be performed at any scale and using equipment from many different manufacturers (e.g., Pharmacia Biotech). Protein concentrations can be determined using any  
20 technique, e.g., as in Bradford (1976) *Anal. Biochem.* 72:248-257.

### *Purification of TRT*

Telomerase can be purified by any of a variety of means provided by the invention, as described above. In one embodiment of the invention, telomerase can be purified to over 60,000-fold purity over cytoplasmic crude cell preparations. Human  
25 TRT can be purified from crude extracts of "293" cells, cells of human embryonic kidney origin that have been transformed with fragments of adenovirus type 5 DNA (Graham (1977) *J. Gen. Virol.* 36:59-77; Stillman (1985) *Mol. and Cell. Biol.* 5:2051-2060). 293 cells are available from the American Type Culture Collection, Accession No. ATCC CRL 1573.

The steps to be included in a purification method depend on the level of purification one desires. A method to purify telomerase enzyme or TRT protein from an impure composition containing organic biomolecules, for example, a crude extract of telomerase positive cells, to at least 60,000-fold compared to crude extract (about 4% relative purity) can, for example, involve: (1) contacting the telomerase or TRT protein with a first matrix that binds molecules bearing a negative charge, for example, POROS 50 HQ, separating telomerase or TRT protein from other organic biomolecules that do not bind to the matrix and collecting the telomerase; (2) contacting the telomerase or TRT protein with a matrix that binds molecules bearing a positive charge, for example, POROS Heparin 20 HE-1, and separating telomerase or TRT protein from other organic biomolecules that do not bind to the matrix and collecting the telomerase; (3) contacting the telomerase or TRT protein with a second matrix that binds molecules bearing a negative charge, for example, SOURCE 15Q, separating telomerase or TRT protein from other organic biomolecules that do not bind to the matrix and collecting the telomerase; (4) contacting the telomerase or TRT protein with an affinity agent having specific affinity for telomerase or a TRT protein or RNA subunit, for example an oligonucleotide complementary to hTR or an anti-TRT or anti-telomerase antibody or other protein, separating telomerase or TRT protein from other organic biomolecules that do not bind to the affinity agent and collecting the telomerase or TRT protein; and (5) separating the telomerase or TRT protein from other organic biomolecules according to molecular size, shape, or buoyant density, for example separating molecules according to size on a TosoHaas TSK-gel\*G5000PW<sub>XL</sub> sizing column and collecting the telomerase or TRT protein. The present invention encompasses protocols comprising fewer or additional steps.

The purification protocol also can include the step of contacting the telomerase or TRT protein with an intermediate-selectivity matrix, separating telomerase from other organic biomolecules that do not bind to the intermediate-selectivity matrix and collecting the telomerase, preferably before the affinity step. Telomerase can be isolated to different levels of purity by altering, changing the sequence of, or eliminating any of the steps in the purification protocol. However, any preferred

protocol will typically include contacting the telomerase with an affinity agent, such as the antibodies of the invention. Contacting the telomerase with at least one matrix that binds molecules bearing a negative charge or a positive charge is typically a preferred step or steps to include in the protocol as well.

5            *Amino Acid Sequence Determination*

Illustrative amino acid sequences of the telomerase, TRT protein and telomerase-associated proteins of this invention can be determined by, for example, Edman degradation, a technique which is well known in the art. In addition to the internal sequencing (see also Hwang (1996) *J. Chromatogr. B. Biomed. Appl.*  
10    686:165-175), N-terminal sequencing can be performed by techniques known in the art. For C-terminal sequence determination, a chemical procedure for the degradation of peptides and analysis by matrix- assisted- laser- desorption ionization mass spectrometry (MALDI-MS) can be used, as described in Thiede (1997) *Eur. J. Biochem.* 244:750-754.

15           *Molecular Weight/Isoelectric Point Determination*

The molecular weight of a protein can be determined by many different methods, all known to one of skill in the art. Some methods of determination include: SDS gel electrophoresis, native gel electrophoresis, molecular exclusion chromatography, zonal centrifugation, mass spectroscopy, and calculation from  
20    sequencing. Disparity between results of different techniques can be due to factors inherent in the technique. For example, native gel electrophoresis, molecular exclusion chromatography and zonal centrifugation depend on the size of the protein. The proteins that are cysteine rich can form many disulfide bonds, both intra- and intermolecular. SDS gel electrophoresis depends on the binding of SDS to amino acids  
25    present in the protein. Some amino acids bind SDS more tightly than others, therefore, proteins will migrate differently depending on their amino acid composition. Mass spectroscopy and calculated molecular weight from the sequence in part depend upon the frequency that particular amino acids are present in the protein and the molecular weight of the particular amino acid. If a protein is glycosylated, mass spectroscopy  
30    results will reflect the glycosylation but a calculated molecular weight may not.

The calculated molecular weight of hTRT (SEQ ID NO:118) was estimated to be about 127 kD. However, additional human or non-human TRT proteins, hTRT, hTRT isoforms and other TRT species within the scope of the invention are not limited to this molecular weight range.

5       The isoelectric point of a protein can be determined by native gel (or disc) electrophoresis, isoelectric focussing or in a preferred method, by calculation given the amino acid content of the protein. The isoelectric point (pI) of hTRT (SEQ ID NO:118) has been calculated to be about 11.3. However, TRT species or isoforms within the scope of the invention are not necessarily limited to this range of isoelectric  
10       points.

      The cDNA clone pGRN121 encodes a functional hTRT (cDNA is SEQ. ID. NO:118) and was isolated from a library of the human 293 cell line as described in Example 17. SEQ. ID. NO: 117 encodes a catalytically active telomerase protein having the sequence of SEQ ID NO:118. The polypeptide of SEQ ID NO:118 has 1132  
15       residues and a calculated molecular weight of about 127 kilodaltons (kD). Comparing clone #712562 (SEQ ID NO:122) with pGRN121 showed that clone #712562 has a 182 base pair deletion between motifs A and B'. The additional 182 basepairs present in pGRN121 places all of the TRT motifs in a single open reading frame, and increases the spacing between the motif A and motif B' regions to a distance consistent with the  
20       other known TRTs.

      TRT can be produced and purified from recombinant sources. For example, host cells transformed with a nucleotide sequence encoding telomerase or telomerase subunit protein(s) may be cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein produced by a  
25       recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing the telomerase or subunit protein encoding sequence can be designed with signal sequences which direct secretion of the telomerase or telomerase subunit protein through a prokaryotic or eukaryotic cell membrane. Other

recombinant constructions may join the sequence encoding the telomerase or subunit protein to a nucleotide sequence encoding a polypeptide domain.

Telomerase or telomerase subunit protein(s) may also be expressed as recombinant proteins with one or more additional polypeptide domains added to facilitate protein purification or other purposes or intended applications. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as polyhistidine tracts and histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequences such as Factor Xa or enterokinase (Invitrogen, San Diego CA) between the purification domain and telomerase or telomerase protein subunits is useful to facilitate purification. One such expression vector provides for expression of a fusion protein comprising the sequence encoding telomerase or telomerase protein subunits and nucleic acid sequence encoding 6 histidine residues followed by thioredoxin and an enterokinase cleavage site. The histidine residues facilitate purification while the enterokinase cleavage site provides a means for purifying the telomerase or telomerase protein subunit from the fusion protein. Literature pertaining to vectors containing fusion proteins is available in the art (*See e.g.*, Kroll *et al.*, DNA Cell. Biol., 12:441-53 [1993]).

#### Chemical Synthesis of TRT Sequences

In an alternate embodiment of the invention, in addition to recombinant production, the sequence encoding the telomerase subunit(s) may be synthesized, whole or in part, using chemical methods well known in the art (*See e.g.*, Caruthers *et al.*, Nucleic Acids Res. Symp. Ser., 215-223 [1980]; and Horn *et al.* Nucleic Acids Res. Symp. Ser., 225-232 [1980]). Alternatively, the protein itself could be produced using chemical methods to synthesize a telomerase subunit amino acid sequence, in whole or in part. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, *et al.* Science 269:202 [1995]; Merrifield, J. Am. Chem. Soc., 85:2149 [1963])) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer) in accordance with the instructions



provided by the manufacturer. Various fragments of a telomerase protein subunit can be chemically synthesized separately and combined using chemical methods to produce a full length or larger molecule.

5 The newly synthesized peptide can be substantially purified by preparative high performance liquid chromatography, as described above (*e.g.*, Creighton, *Proteins, Structures and Molecular Principles*, WH Freeman and Co, New York NY [1983]). The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure; Creighton, *supra*). Additionally the amino acid sequences of telomerase subunit proteins, or any part thereof, may be  
10 altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

Nucleic acids can also be synthetically produced, including oligonucleotide probes and primers, TRT coding sequences, antisense, ribozymes and the like, by a variety of solution or solid phase methods. Detailed descriptions of the procedures for  
15 solid phase synthesis of nucleic acids by phosphite-triester, phosphotriester, and H-phosphonate chemistries are widely available. For example, the solid phase phosphoramidite triester method of Beaucage and Carruthers using an automated synthesizer is described in Itakura, U.S. Pat. No. 4,401,796; Carruthers, U.S. Pat. Nos. 4,458,066 and 4,500,707; Carruthers (1982) *Genetic Engineering* 4:1-17; see also  
20 Needham-VanDevanter (1984) *Nucleic Acids Res.* 12:6159-6168; Beigelman (1995) *Nucleic Acids Res* 23: 3989-3994; Jones, chapt 2, Atkinson, chapt 3, and Sproat, chapt 4, in OLIGONUCLEOTIDE SYNTHESIS: A PRACTICAL APPROACH, Gait (ed.), IRL Press, Washington D.C. (1984); Froehler (1986) *Tetrahedron Lett.* 27:469-472; Froehler, *Nucleic Acids Res.* 14:5399-5407 (1986); Sinha, *Tetrahedron Lett.* 24:5843-5846  
25 (1983); and Sinha, *Nucl. Acids Res.* 12:4539-4557 (1984). Methods to purify oligonucleotides include native acrylamide gel electrophoresis, anion-exchange HPLC, as described in Pearson (1983) *J. Chrom.* 255:137-149. The sequence of the synthetic oligonucleotide can be verified using any chemical degradation method, for example, see Maxam (1980) *Methods in Enzymology* 65:499-560, Xiao (1996) *Antisense Nucleic*

*Acid Drug Dev* 6:247-258, or for solid-phase chemical degradation procedures, Rosenthal (1987) *Nucleic Acids Symp Ser* 18:249-252.

#### Methods Relating to Telomerase and Telomerase Subunit Proteins

5           The nucleotide and peptide sequences disclosed herein are based in part on the homology between the *E. aediculatus* telomerase 123 kDa protein subunit, the yeast protein L8543.12 (Est2), *Schizosaccharomyces*, and the human motifs observed during the development and implementation of and generated by the present invention. In particular, the yeast and 123 kDa protein contain the reverse transcriptase motif in their  
10   C-terminal regions, they share similarity in regions outside the reverse transcriptase motif, they are similarly basic (with a pI of 10.1 for the 123 kDa protein, and of 10.0 for the yeast), and they are both large (123 kDa and 103 kDa). Furthermore, in view of the reverse transcriptase motifs, these subunits are believed to comprise the catalytic core of their respective telomerases. Indeed, the reverse transcriptase motifs of the 123  
15   kDa *E. aediculatus* telomerase protein subunit is shown in the present invention to be useful for the identification of similar sequences in other organisms.

          As *E. aediculatus* and *S. cerevisiae* are so phylogenetically distant, it was contemplated that this homology provided a strong basis for predicting that human and other telomerases will contain a protein that is large, basic, and includes such reverse  
20   transcriptase motifs. Indeed, motifs have been identified within clones encoding the human homolog of the TRT protein. It is further contemplated that this protein is essential for human telomerase catalytic activity. This observation proved valuable for amplification of the human telomerase gene by PCR and other methods. The methods and reagents of the invention have application for screening for telomerase sequences in  
25   human and other animals, as well as for prioritizing candidate telomerase proteins or genes identified by genetic, biochemical, or nucleic acid hybridization methods. It is also contemplated that the telomerase proteins of the present invention will find use in "tailing" or extending chromosomal or other DNA 3' ends *in vitro*.

          It is contemplated that expression of telomerase and/or telomerase subunit  
30   proteins in cell lines will find use in the development of diagnostics for tumors and

aging factors. The nucleotide sequence may be used in hybridization or PCR technologies to diagnose the induced expression of messenger RNA sequences early in the disease process. Likewise the protein can be used to produce antibodies useful in ELISA assays or a derivative or other diagnostic format. Such diagnostic tests allow  
5 different classes of human tumors or other cell-proliferative diseases to be distinguished and thereby facilitate the selection of appropriate treatment regimens.

It is contemplated that the finding of the reverse transcriptase motifs in the telomerase proteins of the present invention will be used to develop methods to test known and yet to be described reverse transcriptase inhibitors, including nucleosides,  
10 and non-nucleosides for anti-telomerase activity.

It is contemplated that the amino acid sequence motifs disclosed herein will lead to the development of drugs (*e.g.*, telomerase inhibitors) useful in humans and/or other animals, that will arrest cell division in cancers or other disorders characterized by proliferation of cells. It is also contemplated that the telomerase proteins will find use  
15 in methods for targeting and directing RNA or RNA-tethered drugs to specific sub-cellular compartments such as the nucleus or sub-nuclear organelles, or to telomeres.

In one embodiment of the diagnostic method of the present invention, normal or standard values for telomerase mRNA expression are established as a baseline. This can be accomplished by a number of assays such as quantitating the amount of  
20 telomerase mRNA in tissues taken from normal subjects, either animal or human, with nucleic probes derived from the telomerase or telomerase protein subunit sequences provided herein (either DNA or RNA forms) using techniques which are well known in the art (*e.g.*, Southern blots, Northern blots, dot or slot blots). The standard values obtained from normal samples may be compared with values obtained from samples  
25 from subjects potentially affected by disease (*e.g.*, tumors or disorders related to aging). Deviation between standard and subject values can establish the presence of a disease state. In addition, the deviation can indicate, within a disease state, a particular clinical outcome (*e.g.*, metastatic or non-metastatic).

The nucleotide sequence encoding telomerase or telomerase protein subunits is  
30 useful when placed in an expression vector for making quantities of protein for

therapeutic use. The antisense nucleotide sequence of the telomerase gene is potentially useful in vectors designed for gene therapy directed at neoplasia including metastases. Additionally, the inhibition of telomerase expression can be useful in detecting the development of disturbances in the aging process or problems occurring during chemotherapy. Alternatively, the telomerase or telomerase protein subunit encoding nucleotide sequences can be used to direct the expression of telomerase or subunits in situations where it is desirable to increase the amount of telomerase activity.

#### **Telomerase Subunit Protein Antibodies**

The invention also provides methods and reagents for detecting or quantitating telomerase and/or TRT or other telomerase subunit protein, such as the *Euplotes* p43 (43 kDa) protein and its human homologue, by a variety of methods. For example, telomerase can be detected and quantified by incorporating functional activity assays of the invention, by immunological assays utilizing a variety of anti-telomerase antibodies provided by the invention, and by nucleic acid-based methodologies, examples of which are also described in detail below.

In one embodiment, the invention provides antibodies that bind hTRT specifically or TRTs generally, and so can be used to identify and isolate any member of the genus of TRTs provided for in the invention or to identify a single specie of telomerase, or hTRT. Antibodies which can identify any member of the genus can be generated by using as antigens peptides containing structural features common to all members of the genus or other TRT-specific epitopes. These common structural features of telomerase are also described above. In general, the antibodies of the invention can be used to identify, purify, or inhibit any or all activity of telomerase enzyme and TRT protein. Antibodies can act as antagonists of telomerase activity in a variety of way, for example, by preventing the telomerase complex or nucleotide from binding to its DNA substrates, by preventing the components of telomerase from forming an active complex, by maintaining a functional (telomerase complex) quaternary structure or by binding to one of the enzyme's active sites or other sites that have allosteric effects on activity (the different partial activities of telomerase are

described in detail elsewhere in this specification). General methods for producing the antibodies of the invention are described below.

It is further contemplated that antibodies directed against the telomerase subunit proteins, including those directed towards TRT motifs, will find use in the diagnosis  
5 and treatment of conditions and diseases associated with expression of telomerase (including the over-expression and the absence of expression).

Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments and fragments produced by a Fab expression library.

10 Given the phylogenetic conservation of the reverse transcriptase motif in the 123 kDa subunit of the *Euplotes* telomerase, it is contemplated that antibodies directed against this subunit will be useful for the identification of homologous subunits in other organisms, including humans, for example, hTRT and the human homologue of the *Euplotes* 43 kDa (p43) TRT polypeptide. It is further contemplated that antibodies  
15 directed against the motifs provided in the present invention will find use in treatment and/or diagnostic areas of application.

Telomerase subunit proteins used for antibody induction need not retain biological activity; however, the protein fragment, or oligopeptide must be immunogenic, and preferably antigenic. Peptides used to induce specific antibodies can  
20 have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids. Preferably, they should mimic a portion of the amino acid sequence of the natural protein and can contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of telomerase subunit protein amino acids can be fused with those of another protein such as keyhole limpet hemocyanin and antibody  
25 produced against the chimeric molecule. Complete telomerase used for antibody induction can be produced by co-expression of protein and RNA components in cells, or by reconstitution *in vitro* from components separately expressed or synthesized.

Methods of producing polyclonal and monoclonal antibodies are known to those of skill in the art and described in the scientific and patent literature, see, e.g., Coligan,  
30 CURRENT PROTOCOLS IN IMMUNOLOGY, Wiley/Greene, NY (1991); Stites (eds.) BASIC

AND CLINICAL IMMUNOLOGY (7th ed.) Lange Medical Publications, Los Altos, CA, and references cited therein ( Stites ); Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE (2d ed.) Academic Press, New York, NY (1986); Kohler (1975) *Nature* 256:495; Harlow and Lane, *supra*. Such techniques include selection of antibodies  
5 from libraries of recombinant antibodies displayed in phage or similar on cells. See, Huse (1989) *Science* 246:1275 and Ward (1989) *Nature* 341:544. Recombinant antibodies can be expressed by transient or stable expression vectors in mammalian cells, as in Norderhaug (1997) *J. Immunol. Methods* 204:77-87.

To produce large amounts of antibodies for use in, for example, immunoaffinity  
10 purification or diagnostics, a number of immunogens provided by the invention may be used. Telomerase purified from a natural source or more preferably from a recombinant protein isolated from transformed cells provided by the present invention can be used as immunogen for the production of monoclonal or polyclonal antibodies. Naturally occurring telomerase or TRT protein from any organism or recombinant  
15 telomerase or TRT protein can be used either in pure or impure form. Synthetic peptides are made using any portion of the TRT amino acid sequence for use as immunogens. The peptides can be used alone or conjugated to another composition as immunogens.

Furthermore, telomere structures can be used as immunogens to create  
20 telomerase-specific antibodies. For example, under certain conditions, telomeres can form higher order superstructures, called G-quartets (Sen (1992) *Biochemistry* 31:65-70; Fang (1993) *Biochemistry* 32:11646-11657) which can be used as immunogens. Other novel tertiary structures which potentially can be immunogenic include stable hairpins or G-quadruplexes by the telomerase product (Salazar (1996) *Biochemistry*  
25 35:16110-16115). These novel structures can act as an immunogens for the formation of antibodies which can, for example, monitor the formation of telomerase product, inhibit telomerase activity or identify telomerase in a sample. These novel structures can also be the hybridization target for nucleotides, which can also be used to measure formation of telomere product, inhibit activity, and the like.

Methods for the production of polyclonal and monoclonal antibodies are known to those of skill in the art. In brief, an immunogen is mixed with an adjuvant, as described above, and animals are immunized. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the immunogen. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done (Harlow and Lane, *supra*). Various illustrative peptides, proteins and fusion proteins of the invention have been used to generate such polyclonal antibodies.

Monoclonal antibodies to telomerase or telomerase protein subunits be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include but are not limited to the hybridoma technique originally described by Koehler and Milstein (Koehler and Milstein, *Nature* 256:495-497 [1975]), the human B-cell hybridoma technique (Kosbor *et al.*, *Immunol. Today* 4:72 [1983]; Cote *et al.*, *Proc. Natl. Acad. Sci.*, 80:2026-2030 [1983]) and the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R Liss Inc, New York NY, pp 77-96 [1985]). Large amounts of monoclonal antibodies for use in immunoaffinity purification or immunoassays may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired telomerase protein are immortalized, commonly by fusion with a myeloma cell. Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for telomerase and TRT protein. The yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from appropriate human B cells, *i.e.*, immunized according to the general protocol outlined in Huse (1989) *Science, supra*.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, etc may be immunized by injection with telomerase protein, protein subunit, or any portion, fragment or oligopeptide which retains immunogenic properties.

Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants are commercially available, and include but are not limited to Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. BCG (*Bacillus Calmette-Guerin*) and *Corynebacterium parvum* are potentially useful adjuvants.

Animals (*e.g.*, inbred strain of mice or rabbits) can be immunized with a TRT or a fragment thereof, such as the polypeptide or peptide comprising SEQ ID NO:118, or with isoforms or immunogenic fragments thereof, alone or using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Polyclonal sera are collected and titered against the telomerase in an immunoassay, for example, a solid phase immunoassay with the telomerase immobilized on a solid support. Polyclonal antisera with a titer of, for example,  $10^4$  or greater are selected and tested for their cross reactivity against homologous proteins from other organisms and/or non-telomerase protein, using, for example, a competitive binding immunoassay. Specific monoclonal and polyclonal antibodies and antisera will usually bind with a  $K_D$  of at least about 1  $\mu\text{M}$ , preferably at least about 0.1  $\mu\text{M}$  or better, and most preferably, 0.01  $\mu\text{M}$  or better.

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening recombinant immunoglobulin libraries or panels of highly specific binding reagents (Orlandi *et al.*, Proc. Natl. Acad. Sci., 86: 3833 [1989]; and Winter and Milstein, Nature 349:293 [1991]).

Antibody fragments which contain specific binding sites for telomerase or telomerase protein subunits may also be generated. For example, such fragments include, but are not limited to, the  $\text{F(ab')}_2$  fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by



reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse *et al.*, Science 256:1275 [1989]).

A variety of protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the formation of complexes between telomerase or telomerase protein subunit and its specific antibody and the measurement of complex formation. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two noninterfering epitopes on a specific telomerase protein subunit is preferred in some situations, but a competitive binding assay may also be employed (See *e.g.*, Maddox *et al.*, J. Exp. Med., 158:1211 [1983]).

Peptides selected from the group comprising the sequences shown in Figure 32 can be used to generate polyclonal and monoclonal antibodies specifically directed against human and other telomerase proteins. The peptides are useful for inhibition of protein-RNA, protein-protein interaction within the telomerase complex, and protein-DNA interaction at telomeres. Antibodies produced against these peptides are then used in various settings, including but not limited to anti-cancer therapeutics capable of inhibiting telomerase activity, for purification of native telomerase for therapeutics, for purification and cloning other components of human telomerase and other proteins associated with human telomerase, and diagnostic reagents.

The concentration of telomerase or TRT protein can be measured by a variety of immunoassay methods of the invention. Generally, immunoassays are described in Stites, *supra*. The immunoassays of the present invention can be performed in any of several configurations, for background information see ENZYME IMMUNOASSAY, E.T. Maggio, ed., CRC Press, Boca Raton, Florida (1980); Tijssen, and Harlow and Lane, *supra*.

#### *Immunological Binding Assays.*

Immunological binding assays (*e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168) are known in the art. For a review, see also METHODS IN CELL BIOLOGY Vol. 37: *Antibodies in Cell Biology*, Asai, ed. Academic Press, Inc. New

York (1993); and Stites, *supra*. Immunological binding assays (or immunoassays) typically utilize a capture agent to bind specifically to and often immobilize the analyte. The capture agent is a moiety that specifically binds to the analyte. In one embodiment of the present invention, the capture agent is an antibody that specifically binds to telomerase or TRT, such antibody (anti-telomerase or anti-TRT) produced by the methods of the present invention.

Immunoassays also often utilize a labeling agent to specifically bind to and label the binding complex formed by the capture agent and the analyte, as described above. The labeling agent may itself be, for example, one of the moieties comprising the antibody/analyte complex: the labeling agent can be a labeled telomerase or a labeled anti-telomerase antibody. Alternatively, the labeling agent may be a third moiety, such as another antibody, that specifically binds to the antibody-telomerase complex. The labeling agent can be, for example, a second anti-telomerase antibody bearing a label. The second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second can be modified with a detectable moiety, such as biotin, to which a third labeled molecule can specifically bind, such as enzyme-labeled streptavidin. Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins are normal constituents of the cell walls of streptococcal bacteria and exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see*, generally Akerstrom (1985) *J. Immunol.* 135:2589-2542; Chaubert (1997) *Mod Pathol* 10:585-591 (1997).

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, preferably from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, analyte, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10EC to 40EC.

(1) *Non-Competitive Assay Formats*

Immunoassays for detecting telomerase and TRT protein may be, for example, either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of captured analyte (as telomerase, TRT or hTRT) is directly  
5 measured. In one preferred "sandwich" assay, for example, the capture agent (anti-telomerase antibodies) can be bound directly to a solid substrate where they are immobilized. These immobilized antibodies then capture protein present in the test sample. The telomerase or TRT protein thus immobilized is then bound by a labeling agent, such as a second anti-telomerase antibody bearing a label. Alternatively, the  
10 second anti-telomerase or anti-TRT antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second can be modified with a detectable moiety, such as biotin, to which a third labeled molecule can specifically bind, such as enzyme-labeled streptavidin.

15 (2) *Competitive Assay Formats*

In competitive assays, the amount of analyte (telomerase) present in the sample is measured indirectly by measuring the amount of an added (exogenous) analyte (telomerase or TRT) displaced (or competed away) from a capture agent (anti-telomerase or anti-TRT antibody) by the analyte present in the sample. In one  
20 competitive assay, a known amount of, in this case telomerase or TRT, usually labeled, is added to the sample and the sample is then contacted with a capture agent, in this case an antibody that specifically binds telomerase or TRT. The amount of labeled telomerase or TRT bound to the antibody is inversely proportional to the concentration of telomerase or TRT present in the sample.

25 In another embodiment, the antibody is immobilized on a solid substrate. The amount of telomerase or TRT bound to the antibody may be determined either by measuring the amount of telomerase or TRT present in an telomerase/antibody or TRT/antibody complex, or alternatively by measuring the amount of remaining uncomplexed telomerase or TRT. The amount of telomerase or TRT may be detected  
30 by providing a labeled telomerase or TRT molecule.

A hapten inhibition assay is another competitive assay. In this assay a known analyte, in this invention telomerase or TRT, is immobilized on a solid substrate. A known amount of anti-telomerase or anti-TRT antibody is added to the sample, and the sample is then contacted with the immobilized telomerase or TRT. In this case, the amount of anti-telomerase or anti-TRT antibody bound to the immobilized telomerase or TRT is inversely proportional to the amount of telomerase or TRT present in the sample. Again the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

Immunoassays in the competitive binding format can be used for crossreactivity determinations to permit one of skill to determine if a protein or enzyme complex is a TRT or telomerase enzyme of the invention. For example, a TRT can be immobilized to a solid support. Proteins are added to the assay which compete with the binding of the antisera to the immobilized antigen. The ability of the proteins to compete with the binding of the antisera to the immobilized TRT is compared to the binding by the same TRT as was used to coat the solid support.

### (3) Other Assay Formats

The present invention also provides methods for Western blot (immunoblot) analysis to detect and/or quantify the presence of telomerase protein in a sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind telomerase. The anti-telomerase protein antibodies specifically bind to telomerase on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-telomerase protein.

Antibodies can also be used to probe expression libraries, see Young (1982) *Proc. Natl. Acad. Sci. USA* 80:1194. In general, a cDNA expression library may be prepared from commercially available kits or using readily available components. Phage (Hurst (1997) *Methods Mol Biol* 69:155-159), bacteria (Davis (1997) *Proc. Natl. Acad. Sci. USA* 94:2128-2132), insect (Granziero (1997) *J. Immunol. Methods* 203:131-139), yeast, and animal cell libraries (*Xenopus* oocytes) can be used. One selects mRNA from a source that is optionally enriched with the target mRNA or in which the protein is abundant and creates cDNA which is then ligated into a vector and the vector is transformed into the library host cells for immunoscreening. Screening involves binding and identification of antibodies bound to specific proteins on cells or immobilized on a solid support such as nitrocellulose or nylon membranes. Positive clones are selected for purification to homogeneity and the isolated cDNA then prepared for expression in the desired host cells. See also METHODS OF CELL BIOLOGY, VOL. 37, *Antibodies in Cell Biology*, Assai (ed.) 1993.

The methods of the invention are also compatible with other assay formats, including liposome immunoassays (LIA) (Rongen (1997) *J. Immunol. Methods* 204:105-133), in which liposomes designed to bind specific molecules (e.g., antibodies) and release encapsulated reagents or markers are employed. The released chemicals can be detected using standard techniques (see, e.g. Monroe (1986) *Amer. Clin. Prod. Rev.* 5:34 ).

#### **Diagnostic Assays Using Telomerase Specific Antibodies**

Particular telomerase and telomerase protein subunit antibodies are useful for the diagnosis of conditions or diseases characterized by expression of telomerase or telomerase protein subunits, or in assays to monitor patients being treated with telomerase, its fragments, agonists or inhibitors (including antisense transcripts capable of reducing expression of telomerase). Diagnostic assays for telomerase include methods utilizing the antibody and a label to detect telomerase in human body fluids or extracts of cells or tissues. The polypeptides and antibodies of the present invention can be used with or without modification. Frequently, the polypeptides and antibodies

will be labeled by joining them, either covalently or noncovalently, with a reporter molecule. A wide variety of reporter molecules are known, several of which were described above. In particular, the present invention is useful for diagnosis of human disease, although it is contemplated that the present invention will find use in the  
5 veterinary arena.

A variety of protocols for measuring telomerase protein(s) using either polyclonal or monoclonal antibodies specific for the respective protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and fluorescent activated cell sorting (FACS). A two-site,  
10 monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on the telomerase proteins or a subunit is preferred, but a competitive binding assay can be employed. These assays are described, among other places, in Maddox (Maddox *et al.*, J. Exp. Med., 158:1211 [1983]).

In order to provide a basis for diagnosis, normal or standard values for human  
15 telomerase expression are usually established. This is accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with antibody to telomerase or telomerase subunit(s) under conditions suitable for complex formation which are well known in the art. The amount of standard complex formation is quantified by comparing various artificial membranes containing known quantities of  
20 telomerase protein, with both control and disease samples from biopsied tissues. Then, standard values obtained from normal samples are compared with values obtained from samples from subjects potentially affected by disease (*e.g.*, metastases). Deviation between standard and subject values establishes the presence of a disease state.

**Drug Screening**

The invention contemplates screening for compositions capable of modifying the DNA replicative capacity of telomerase, or a partial activity of telomerase or TRT, by any means. In various embodiments, the invention includes: screening for

5 antagonists that bind to TRT protein's active site or interfere with reverse transcription of its RNA moiety; screening for compositions that inhibit the association of nucleic acid and/or telomerase-associated compositions with TRT, such as the association of TR with TRT or the association of TRT with a telomerase associated protein, or association of TRT with a telomere or a nucleotide; screening for compositions that

10 promote the disassociation or promote the association of the enzyme complex, such as an antibody directed to TR or TRT; screening for agents that effect the processivity of the enzyme; and, screening for nucleic acids and other compositions that bind to TRT, such as a nucleic acid identical or complementary to TR. The invention further contemplates screening for compositions that increase or decrease the transcription of

15 the TRT gene and/or translation of the TRT gene product.

Screening for antagonist activity provides for compositions that decrease telomerase replicative capacity, thereby mortalizing otherwise immortal cells, such as cancer cells. Telomerase activity has been identified as an important cancer marker, one whose levels can detect, diagnose and prognose the outcome or seriousness of

20 disease, as described in U.S. Patent Nos. 5,489,508; 5,648,125; and 5,639,613. The present invention provides useful reagents for diagnosing and prognosing cancer by analyzing a telomerase activity and hTRT gene expression.

Screening for agonist activity or transcriptional or translational activators provides for compositions that increase the telomerase's telomere replicative capacity,

25 or a partial activity. Such agonist compositions provide for methods of immortalizing otherwise normal untransformed cells, including cells which can express useful proteins. Such agonists can also provide for methods of controlling cellular senescence.

Telomerase or telomerase subunit proteins or their catalytic or immunogenic

30 fragments or oligopeptides thereof can be used for screening therapeutic compounds in

any of a variety of drug screening techniques. The fragment employed in such a test may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes, between telomerase or the subunit protein and the agent being tested, may be measured.

5           Another technique for drug screening which may be used for high throughput screening of compounds having suitable binding affinity to the telomerase or telomerase protein subunit is described in detail in "Determination of Amino Acid Sequence Antigenicity" (Geysen, WO Application 84/03564, published on September 13, 1984, incorporated herein by reference). In summary, large numbers of different  
10   small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with fragments of telomerase or telomerase protein subunits and washed. Bound telomerase or telomerase protein subunit is then detected by standard methods developed for other applications well known in the art. Substantially purified telomerase or telomerase protein subunit  
15   can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

          This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding telomerase or subunit protein(s)  
20   specifically compete with a test compound for binding telomerase or the subunit protein. In this manner, the antibodies can be used to detect the presence of any peptide which shares with the antibody the ability to bind one or more antigenic determinants with the telomerase or subunit protein.

#### 25   **Polynucleotides Encoding Telomerase Subunit Proteins and Their Applications**

          A polynucleotide sequence encoding telomerase subunit proteins or any part thereof may be used for diagnostic and/or therapeutic purposes. For diagnostic purposes, the sequence encoding a telomerase subunit protein of this invention can be used to detect and quantitate gene expression of the telomerase or subunit protein. The  
30   diagnostic assay is useful to distinguish between absence, presence, and excess



expression of telomerase, and to monitor regulation of telomerase levels during therapeutic intervention. Included in the scope of the invention are oligonucleotide sequences, antisense RNA and DNA molecules, and synthetic and non-naturally occurring analogues thereof, including, for example, nucleotides with non-ionic  
5 backbones, such as peptide nucleic acids (PNAs).

Another aspect of the subject invention is to provide hybridization or PCR probes or primers that are capable of detecting polynucleotide sequences, including genomic sequences, encoding telomerase subunit proteins or closely related molecules. The specificity of the probe, whether it is made from a highly specific region (*e.g.*, 10  
10 unique nucleotides in the 5' regulatory region), or a less specific region (*e.g.*, especially in the 3' region), and the stringency of the hybridization or amplification (maximal, high, intermediate or low) will determine whether the probe identifies only naturally occurring telomerase, telomerase subunit proteins or related sequences of a particular telomerase or TRT species or all or some of the members of the genus of TRT  
15 polynucleotides.

Probes may also be used for the detection of related sequences and should preferably contain at least 50% of the nucleotides (identical or complementary) from any of these telomerase subunit protein-encoding sequences. The hybridization probes of the subject invention may be derived from the nucleotide sequence provided by the  
20 present invention (*e.g.*, SEQ ID NO:1, 3, 62, 66, 69, or 117), or from genomic sequences including promoter, enhancer elements and introns of the naturally occurring sequences encoding telomerase subunit proteins. Hybridization probes may be labeled by a variety of reporter groups, including commercially available radionuclides such as <sup>32</sup>P or <sup>35</sup>S, or enzymatic labels such as alkaline phosphatase coupled to the probe via  
25 avidin/biotin coupling systems, and the like.

Other means for producing specific hybridization probes for DNAs include the cloning of nucleic acid sequences encoding telomerase subunit proteins or derivatives into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by

means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides.

### **Diagnostic Applications**

5 Polynucleotide sequences encoding telomerase may be used for the diagnosis of conditions or diseases with which the abnormal expression of telomerase is associated. For example, polynucleotide sequences encoding human telomerase may be used in hybridization or PCR assays of fluids or tissues from biopsies to detect telomerase expression. The form of such qualitative or quantitative methods may include Southern  
10 or northern analysis, dot blot or other membrane-based technologies; PCR technologies; dip stick, pin, chip and ELISA technologies. All of these techniques are well known in the art and are the basis of many commercially available diagnostic kits.

The telomerase-encoding nucleotide sequences disclosed herein provide the basis for assays that detect activation or induction associated with disease (including  
15 metastasis); in addition, the lack of expression of telomerase may be detected using the telomerase-encoding nucleotide sequences disclosed herein. The nucleotide sequence may be labeled by methods known in the art and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After an incubation period, the sample is washed with a compatible fluid which optionally  
20 contains a dye (or other label requiring a developer) if the nucleotide has been labeled with an enzyme. After the compatible fluid is rinsed off, the dye is quantitated and compared with a standard. If the amount of dye in the biopsied or extracted sample is significantly elevated over that of a comparable control sample, the nucleotide sequence has hybridized with nucleotide sequences in the sample, and the presence of elevated  
25 levels of nucleotide sequences encoding telomerase in the sample indicates the presence of the associated disease. Alternatively, the loss of expression of human telomerase sequences in a tissue which normally expresses telomerase sequences indicates the presence of an abnormal or disease state.

Such assays may also be used to evaluate the efficacy of a particular therapeutic  
30 treatment regime in animal studies, in clinical trials, or in monitoring the treatment of

an individual patient. In order to provide a basis for the diagnosis of disease, a normal or standard profile for human telomerase expression must be established. This is accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with human telomerase or a portion thereof, under conditions  
5 suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained for normal subjects with a dilution series of human telomerase run in the same experiment where a known amount of substantially purified human telomerase is used. Standard values obtained from normal samples may be compared with values obtained from samples from patients affected by  
10 telomerase-associated diseases. Deviation between standard and subject values establishes the presence of disease.

Once disease is established, a therapeutic agent is administered and a treatment profile is generated. Such assays may be repeated on a regular basis to evaluate whether the values in the profile progress toward or return to the normal or standard  
15 pattern. Successive treatment profiles may be used to show the efficacy of treatment over a period of several days or several months.

PCR, which may be used as described in US Patent Nos. 4,683,195, 4,683,202, and 4,965,188 (herein incorporated by reference) provides additional uses for oligonucleotides based upon the sequence encoding telomerase subunit proteins. Such  
20 oligomers are generally chemically synthesized, but they may be generated enzymatically or produced from a recombinant source. Double-stranded nucleic acids comprise two separate strands of nucleotide sequences, one with sense orientation (5' to 3') and one with antisense (3' to 5'), and can also be employed under optimized conditions for identification of a specific gene or condition. Oligomers, nested sets of  
25 oligomers, or even a degenerate pool of oligomers may be employed under less stringent conditions for detection and/or quantitation of closely related DNA or RNA sequences.

Additionally, methods which may be used to quantitate the expression of a particular molecule include radiolabeling (Melby *et al.*, J. Immunol. Meth., 159:235-44  
30 [1993]) or biotinylating [Duplaa *et al.*, Anal. Biochem., 229-36 [1993]) nucleotides, co-

amplification of a control nucleic acid, and standard curves onto which the experimental results are interpolated. Quantitation of multiple samples may be speeded up by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid  
5 quantitation. A definitive diagnosis of this type may allow health professionals to begin aggressive treatment and prevent further worsening of the condition. Similarly, further assays can be used to monitor the progress of a patient during treatment. Furthermore, the nucleotide sequences disclosed herein may be used in molecular biology techniques that have not yet been developed, provided the new techniques rely  
10 on properties of nucleotide sequences that are currently known such as the triplet genetic code, specific base pair interactions, and the like.

#### **Therapeutic Application**

Based upon its homology to other telomerase sequences, the polynucleotides  
15 encoding telomerase protein subunits disclosed herein can be useful in the treatment of metastasis; in particular, inhibition of telomerase expression may be therapeutic.

Expression vectors derived from retroviruses, adenovirus, herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences (sense or antisense) to the targeted organ, tissue or cell population. Methods  
20 which are well known to those skilled in the art can be used to construct recombinant vectors which will express antisense of a sequence encoding a telomerase subunit. See, for example, the techniques described in Sambrook *et al.* (*supra*) and Ausubel *et al.* (*supra*).

The polynucleotides comprising full length cDNA sequence and/or its  
25 regulatory elements enable researchers to use the sequence encoding a telomerase subunit, including the various motifs as an investigative tool in sense (Youssoufian and Lodish, Mol. Cell. Biol., 13:98-104 [1993]) or antisense (Eguchi *et al.*, Ann. Rev. Biochem., 60:631-652 [1991]) regulation of gene function. Such technology is now well known in the art, and sense or antisense oligomers, or larger fragments, can be  
30 designed from various locations along the coding or control regions.

Genes encoding a telomerase subunit can be turned off by transfecting a cell or tissue with expression vectors which express high levels of a desired telomerase fragment. Such constructs can flood cells with untranslatable sense or antisense sequences. Even in the absence of integration into the DNA, such vectors may continue  
5 to transcribe RNA molecules until all copies are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector and even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing antisense molecules, DNA, RNA, PNA, or the like, to the control regions of  
10 the sequence encoding human telomerase (*i.e.*, the promoters, enhancers, and introns). Oligonucleotides derived from the transcription initiation site, (e.g., between -10 and +10 regions of the leader sequence) are preferred for some applications. The antisense molecules may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes. Similarly, inhibition can be achieved using  
15 "triple helix" base-pairing methodology. Triple helix pairing compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules (for a review of recent therapeutic advances using triplex DNA, see Gee *et al.*, in Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co, Mt Kisco NY [1994]).

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#### **Inhibitory Oligonucleotides**

One particularly useful set of inhibitors provided by the present invention includes oligonucleotides which are able to either bind mRNA encoding TRT protein or to the TRT gene, in either case preventing or inhibiting the production of functional  
25 TRT protein. Other oligonucleotides of the invention interact with telomerase's RNA moiety, such as hTR, or are able to prevent binding of telomerase or TRT to its DNA target, or one telomerase component to another, or to a substrate. Such oligonucleotides can also bind the telomerase enzyme or TRT protein and inhibit a partial activity as described above (such as its processive activity, its reverse  
30 transcriptase activity, its nucleolytic activity, and the like). The association can be

though sequence specific hybridization to another nucleic acid or by general binding, as in an aptamer.

Another useful class of inhibitors includes oligonucleotides which cause inactivation or cleavage of hTRT mRNA or hTR. That is, the oligonucleotide is chemically modified or has enzyme activity which causes such cleavage, such as ribozymes. As noted above, one may screen a pool of many different such oligonucleotides for those with the desired activity.

Another useful class of inhibitors includes oligonucleotides which bind polypeptides. Double- or single-stranded DNA or single-stranded RNA molecules that bind to specific polypeptides targets are called "aptamers." The specific oligonucleotide-polypeptide association may be mediated by electrostatic interactions. For example, aptamers specifically bind to anion-binding exosites on thrombin, which physiologically binds to the polyanionic heparin (Bock (1992) *Nature* 355:564-566). Because TRT protein binds both hTR and its DNA substrate, and because the present invention provides hTRT and other TRT proteins in purified form in large quantities, those of skill in the art can readily screen for TRT-binding aptamers using the methods of the invention.

Antagonists of telomerase-mediated DNA replication can also be based on inhibition of TR, such as hTR (Norton (1996) *Nature Biotechnology* 14:615-619) through complementary sequence recognition or cleavage, as through ribozymes. Such agents can be used in combination with those of the invention to enhance the desired effect.

Telomerase activity can be inhibited by targeting the TRT mRNA with antisense oligonucleotides capable of binding the TRT mRNA. In some situations, naturally occurring nucleic acids used as antisense oligonucleotides may need to be relatively long (18 to 40 nucleotides) and present at high concentrations. A wide variety of synthetic, non-naturally occurring nucleotide and nucleic acid analogues are known which can address this potential problem. For example, as discussed above, PNAs containing non-ionic backbones, such as N-(2-aminoethyl) glycine units can be used. Antisense oligonucleotides having phosphorothioate linkages can also be used, as

described in WO 97/03211; WO 96/39154; Mata (1997) *Toxicol Appl Pharmacol* 144:189-197; Antisense Therapeutics, ed. Sudhir Agrawal (Humana Press, Totowa, New Jersey, 1996). Antisense oligonucleotides having synthetic DNA backbone analogues provided by the invention can also include phosphoro-dithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-carbamate, and morpholino carbamate nucleic acids, as described above.

As noted above, combinatorial chemistry methodology can be used to create vast numbers of oligonucleotides that can be rapidly screened for specific oligonucleotides that have appropriate binding affinities and specificities toward any target, such as the TRT proteins of the invention (for general background information, see Gold (1995) *J. of Biol. Chem.* 270:13581-13584).

#### **Inhibitory Ribozymes**

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Within the scope of the invention are engineered hammerhead motif ribozyme molecules that can specifically and efficiently catalyze endonucleolytic cleavage of the sequence encoding human telomerase.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Ribozymes act by binding to a target RNA through the target RNA binding portion of a ribozyme which is held in close proximity to an enzymatic portion of the

RNA that cleaves the target RNA. Thus, the ribozyme recognizes and binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cleave and inactivate the target RNA. Cleavage of a target RNA in such a manner will destroy its ability to direct synthesis of an encoded protein if the cleavage occurs in the coding sequence. After a ribozyme has bound and cleaved its RNA target, it is typically released from that RNA and so can bind and cleave new targets repeatedly.

In some circumstances, the enzymatic nature of a ribozyme can be advantageous over other technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its transcription, translation or association with another molecule) as the effective concentration of ribozyme necessary to effect a therapeutic treatment can be lower than that of an antisense oligonucleotide. This potential advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, a ribozyme is typically a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding, but also on the mechanism by which the molecule inhibits the expression of the RNA to which it binds. That is, the inhibition is caused by cleavage of the RNA target and so specificity is defined as the ratio of the rate of cleavage of the targeted RNA over the rate of cleavage of non-targeted RNA. This cleavage mechanism is dependent upon factors additional to those involved in base pairing. Thus, the specificity of action of a ribozyme can be greater than that of antisense oligonucleotide binding the same RNA site.

The enzymatic ribozyme RNA molecule has complementarity to the target, such as the mRNA encoding TRT. The enzymatic ribozyme RNA molecule is able to cleave RNA and thereby inactivate a target RNA molecule. The complementarity functions to allow sufficient hybridization of the enzymatic ribozyme RNA molecule to the target RNA for cleavage to occur. One hundred percent complementarity is preferred, but complementarity as low as 50-75% may also be employed. The present invention provides ribozymes targeting any portion of the coding region for a TRT gene that



cleave the TRT gene mRNA in a manner that will inhibit the translation of the mRNA and thus reduce telomerase activity. In addition, the invention provides ribozymes targeting the nascent RNA transcript of the TRT gene to reduce telomerase activity.

The enzymatic ribozyme RNA molecule can be formed in a hammerhead motif, but may also be formed in the motif of a hairpin, hepatitis delta virus, group I intron or RNaseP-like RNA (in association with an RNA guide sequence). Examples of such hammerhead motifs are described by Rossi (1992) *Aids Research and Human Retroviruses* 8:183; hairpin motifs by Hampel (1989) *Biochemistry* 28:4929, and Hampel (1990) *Nuc. Acids Res.* 18:299; the hepatitis delta virus motif by Perrotta (1992) *Biochemistry* 31:16; the RNaseP motif by Guerrier-Takada (1983) *Cell* 35:849; and the group I intron by Cech U.S. Pat. No. 4,987,071. The recitation of these specific motifs is not intended to be limiting; those skilled in the art will recognize that an enzymatic RNA molecule of this invention has a specific substrate binding site complementary to one or more of the target gene RNA regions, and has nucleotide sequences within or surrounding that substrate binding site that impart an RNA cleaving activity to the molecule.

Antisense molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of RNA molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding human telomerase and/or telomerase protein subunits. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly can be introduced into cell lines, cells or tissues.

RNA molecules can be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these

molecules by the inclusion of nontraditional bases such as inosine, queosine and wybutosine as well as acetyl-, methyl-, thio- and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

5           Methods for introducing vectors into cells or tissues include those methods discussed *infra*, and which are equally suitable for *in vivo*, *in vitro* and *ex vivo* therapy. For *ex vivo* therapy, vectors can be introduced into cells, such as stem cells, taken from the patient and clonally propagated for autologous transplant back into that same patient, as is presented in a different context in US Patent Nos. 5,399,493 and  
10   5,437,994, the disclosure of which is herein incorporated by reference. Delivery by transfection and by liposome are quite well known in the art and applicable to the present invention.

#### Detection and Mapping of Related Polynucleotide Sequences

##### 15   in Other Genomes

          The nucleic acid sequence encoding *E. aedicularis*, *S. cerevisiae*, *S. pombe*, and human telomerase subunit proteins and sequence variants thereof, can also be used to generate hybridization probes for mapping the naturally occurring homologous genomic sequence in human and other genomes. The sequence may be mapped to a  
20   particular chromosome or to a specific region of the chromosome using well known techniques. These include *in situ* hybridization to chromosomal spreads, flow-sorted chromosomal preparations, or artificial chromosome constructions such as yeast artificial chromosomes, bacterial artificial chromosomes, bacterial P1 constructions or single chromosome cDNA libraries, as reviewed by Price (Price, Blood Rev., 7:127  
25   [1993]) and Trask (Trask, Trends Genet 7:149 [1991]).

          The technique of fluorescent *in situ* hybridization (FISH) of chromosome spreads has been described (Verma *et al.*, *Human Chromosomes: A Manual of Basic Techniques*, Pergamon Press, New York NY [1988]). Fluorescent *in situ* hybridization  
30   of chromosomal preparations and other physical chromosome mapping techniques can be correlated with additional genetic map data. Examples of genetic map data can be

found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of the sequence encoding a telomerase unit protein on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with the disease. The nucleotide sequences of the subject  
5 invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

*In situ* hybridization of chromosomal preparations and physical mapping techniques such as linkage analysis using established chromosomal markers are invaluable in extending genetic maps (See e.g., Hudson *et al.*, Science 270:1945  
10 [1995]). Often the placement of a gene on the chromosome of another mammalian species such as mouse (Whitehead Institute/MIT Center for Genome Research, Genetic Map of the Mouse, Database Release 10, April 28, 1995) may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms, or parts thereof, by physical  
15 mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques.

### **Optimizing Expression of Telomerase and TRT**

In bacterial and other expression systems, codon usage is known to present a  
20 potential impediment to high-level gene expression. "Rare" codons, depending on their frequency and context in an mRNA, can have an adverse effect on levels of protein translated therefrom. The problem, if encountered, can be alleviated by modification of the relevant codons or by coexpression of the cognate tRNA genes or by other means. Use of protease-deficient host strains can also increase yields from bacterial expression  
25 systems, see Makrides (1996) *Microbiol Rev* 60:512-538.

One can optimize levels of expression of telomerase and TRT by vector design modifications, such as using exogenous transcriptional regulatory elements. For example, as discussed below, the myeloproliferative sarcoma virus (MPSV) LTR promoter consistently drives higher expression levels in some mammalian cell lines.

Generally, those of skill in the art recognize that nucleic acids having certain specific sequences can be poorly expressed in one cell and expressed well in other cells. As a precaution, one should avoid including extraneous sequences, *i.e.*, non-coding sequences such as 3' untranslated sequences from a cDNA, with the desired coding sequence. Thus, one optimization strategy involves removing all extraneous sequences from the coding sequence insert. This strategy can in some circumstances increase protein expression 5 to 10 fold in bacteria, insect, yeast, mammalian and other cells expression systems.

Gene amplification, whether by higher vector copy number or by replication of a gene in a chromosome, can increase yields of recombinant proteins in mammalian and other cells. One *in vitro* amplification method for heterologous gene expression in mammalian cells is based on the stable transfection of cells with long, linear DNA molecules having several copies of complete expression units, coding for the gene of interest, linked to one terminal unit coding for a selectable marker. As another example, gene amplification of the gene of interest can be achieved by linking it to a dihydrofolate reductase (Dhfr) gene and administering methotrexate to the transfected cells; this method can increase recombinant protein production many fold (see Monaco (1996) *Gene* 180:145-150).

## **20      Production and Expression of and Screening with Telomerase and TRT**

In one embodiment, the invention provides screening assays to identify modulators of telomerase activity in animals and plants. The screening assay can utilize telomerase or TRT derived by a full or partial reconstitution of telomerase activity, or by an augmentation of existing activity. The assay or screens provided by the invention can be used to test for the ability of telomerase to synthesize telomere DNA or to test for any one or all or of the "partial activities" of TRT and TRTs generally, as described above. The assay can incorporate *ex vivo* modification of cells which have been manipulated to express telomerase with or without its RNA moiety or associated proteins, and these can be reimplanted into an animal, which can be used for *in vivo* testing. Thus, this invention provides *in vivo* assays and transgenic animals

useful therein. These *in vivo* assays systems can employ "knockout" cells, in which one or several units of the endogenous telomerase enzyme complex have been deleted or inhibited, as well as cells in which an exogenous or endogenous telomerase activity is reconstituted or activated.

5       The invention also contemplates a method of screening for telomerase modulators in animals by reconstituting a telomerase activity, or an anti-telomerase activity, into an animal, such as a transgenic animal. The invention provides for *in vivo* assays systems that include "knockout" models, in which one or several units of the endogenous telomerase, such as TRT, telomerase RNA moiety and/or telomerase-  
10       associated proteins have been deleted or inhibited. The endogenous telomerase activity, full or partial, can remain. The "knockout" of such genes includes knocking out of cell lines, tissues, or entire animals, as with transgenic animals.

      In one embodiment, an exogenous telomerase activity, full or partial, is reconstituted. The transgenic animals of the invention also provide for methods of  
15       expressing large amounts of fully or partially active telomerase compositions of the invention. Transgenic animals also provide for immortalization of otherwise normal cells, which can then be used to express compositions of interest.

      In one embodiment of the invention, recombinant telomerase is expressed in normal, diploid mortal cells to immortalize them, or to facilitate long-term culture or  
20       replication of the cells. Other telomerase enzyme complex components, such as nucleic acid telomeric sequence template molecules (hTR, for example) or other associated proteins, that are beneficial for expression or act as modulators of activity, can also be co-expressed. This invention provides methods to obtain diploid immortal cells with an otherwise normal phenotype and karyotype. This aspect of the invention is of  
25       enormous practical and commercial utility; for example, the FDA and public would value the production of recombinant proteins from normal cells to minimize concern regarding viral or other contamination of the products made from such cells. The present invention allows one to produce immortal hybrids of human B lymphocytes and myeloma cells to obtain human hybridomas for human monoclonal antibody  
30       production. Using the methods of this invention, transfection of TRT protein and

telomerase activity into human B lymphocytes allows one to generate immortal cells for antibody production. Another embodiment provides for methods for introducing recombinant telomerase and/or telomerase associated RNA and other compounds of the invention into cells to produce a commercially desirable protein. For example, by the methods of the invention an immortal, yet karyotypically normal, human pituitary cell that makes hormones, such as growth hormone, could be produced for commercial use. In a variation of this embodiment, a normal human cell is removed from the body, immortalized using the methods and reagents of the invention, transfected with a gene of interest such that the gene is expressed at appropriate levels and introduced back into the individual such that the transfected gene expresses a molecule that impacts the health of the individual.

Another embodiment of the invention involves a similar method, but the cell is a "universal donor cell" which has been modified to delete histocompatibility antigens or modified in some way to prevent or decrease the possibility of immune rejection. A complication arising from the reintroduction of these cells into an individual is the possibility that the cells may lose growth control and change to a state of uncontrolled cell growth, becoming a cancer, tumor or other malignancy. The present invention solves this complication by providing means to express TRT or other telomerase components conditionally and/or by providing means for knocking out the telomerase (or a telomerase enzyme complex component necessary for activity). Moreover, even "mortal" cells used in transplantation or for other purposes can be mortalized by the methods of the invention. Without an active telomerase, the cells are irreversibly mortal, thus decreasing the probability of cancerous or malignant transformation after transplantation or other reintroduction into a host organism. This would not affect the cell's function, as telomerase is not normally active in somatic cells.

Means to provide TRT and other telomerase components conditionally, *i.e.*, controllable expression in the host cell, tissue or animal, includes use of antisense constructs which, when signaled to express the antisense nucleotide in the appropriate cell or tissue, inhibits telomerase activity and stops the cell from dividing. Expression of recombinant antibody binding components intracellularly can also be used for this

purpose. Inducible and/or tissue-specific cis- and/or trans-acting transcriptional and translational regulatory elements can be used to control expression of TRT and other telomerase components. Examples of cis-acting transcriptional regulatory elements include promoters and enhancers of the telomerase gene. Examples of cis-acting  
5 translational regulatory elements include elements that stabilize mRNA or protect the transcript from degradation. The identification and isolation of cis- and trans- acting regulatory agents provide for further methods and reagents for identifying agents that modulate transcription and translation of telomerase.

The invention also provides transgenic animals and methods for expressing the  
10 telomerase and TRT compositions of the invention in such animals, as well as otherwise normal cells that can be used to express compositions of interest and can be used in related methods. The invention also provides transgenic animals expressing endogenous or exogenous TRT, either alone or co-expressed with the enzyme's RNA moiety or other telomerase-associated proteins. The invention provides for transgenic  
15 animals and recombinant cells to be used, for example, as bioreactors (Khillan (1997) *Methods Mol. Biol.* 63:327-342) to produce large amounts of telomerase, TRT and other proteins of the invention. To create a living assay system to screen for modulators of TRT, a non-human animal model can be used. In this non-human animal, the endogenous telomerase can be first debilitated, or "knocked out" before  
20 introducing a recombinant TRT, TR and/or other telomerase-associated components.

Telomerase-expressing nucleic acid of the invention may be introduced into the genome of an animal or plant host organism by a variety of conventional techniques (Jacenko (1997) *Methods Mol Biol* 62, 399-424). For example, recent advances in transgenic and gene-targeting approaches allow a sophisticated manipulation of the  
25 mouse genome by gene addition, gene deletion, or gene modifications, making this animal convenient for the methods of the invention (Franz (1997) *J Mol Med* 75:115-129; Peterson (1997) *Genet. Eng. (NY)* 19:235-255). Many cloning vectors for transgene construction are known in the art, for example, as in Yang (1997) *Biotechniques* 22:1032-1034. There are two well-established procedures for simple  
30 introduction of DNA into animal genomes, pronuclear DNA injection and transduction

using a retrovirus (Wei (1997) *Annu. Rev. Pharmacol. Toxicol.* 37:119-141).

Microinjection techniques for use in introducing DNA into animals and plants are known in the art and described in the scientific and patent literature. The introduction of DNA constructs into cells using polyethylene glycol precipitation is described in  
5 Paszkowski (1984) *EMBO J.* 3:2717. Electroporation techniques are described in Fromm (1985) *Proc. Natl. Acad. Sci. USA* 82:5824. Ballistic transformation techniques are described in Klein (1987) *Nature* 327:70.

The invention also provides transgenic plants and methods for expressing the telomerase and TRT compositions of the invention and screening assays to identify  
10 modulators of telomerase activity in such plants. In plants, the DNA construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the DNA constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. As discussed above, plant virus vectors such as tobacco mosaic virus  
15 containing the telomerase sequences of the invention can be used to inoculate a plant (Rouwendal (1997) *Plant Mol Biol* 33:989-999).

### **Pharmaceutical Compositions**

The present invention also relates to pharmaceutical compositions that comprise  
20 telomerase and/or telomerase subunit nucleotides, proteins, antibodies, agonists, antagonists, or inhibitors, alone or in combination with at least one other agent, such as a stabilizing compound, which can be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. Any of these molecules can be administered to a patient alone, or in  
25 combination with other agents, drugs or hormones, in pharmaceutical compositions where it is mixed with suitable excipient(s), adjuvants, and/or pharmaceutically acceptable carriers. In one embodiment of the present invention, the pharmaceutically acceptable carrier is pharmaceutically inert.



**Administration Of Pharmaceutical Compositions**

Administration of pharmaceutical compositions is accomplished orally or parenterally. Methods of parenteral delivery include topical, intra-arterial (*e.g.*, directly to the tumor), intramuscular, subcutaneous, intramedullary, intrathecal, intraventricular, 5 intravenous, intraperitoneal, or intranasal administration. In addition to the active ingredients, these pharmaceutical compositions can contain suitable pharmaceutically acceptable carriers comprising excipients and other compounds that facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration can 10 be found in the latest edition of "Remington's Pharmaceutical Sciences" (Maack Publishing Co, Easton PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated 15 as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, etc., suitable for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable additional compounds, if 20 desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers include, but are not limited to sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; and gums including arabic and tragacanth; as well as proteins 25 such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores are provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, 30 polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic

solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound (*i.e.*, dosage).

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds can be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations for parenteral administration include aqueous solutions of active compounds. For injection, the pharmaceutical compositions of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions can contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds can be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension can also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

#### **Manufacture And Storage**

The pharmaceutical compositions of the present invention can be manufactured in substantial accordance with standard manufacturing procedures known in the art

(*e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes).

The pharmaceutical composition can be provided as a salt and can be formed with many acids, including but not limited to hydrochloric, sulfuric, acetic, lactic, 5 tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents that are the corresponding free base forms. In other cases, the preferred preparation can be a lyophilized powder in 1 mM-50 mM histidine, 0.1%-2% sucrose, 2%-7% mannitol at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions comprising a compound of the invention 10 formulated in a acceptable carrier have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. Such labeling would typically include amount, frequency and method of administration.

#### **Therapeutically Effective Dose**

15 Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially 20 either in cell culture assays or in an appropriate animal model. The animal model is also used to achieve a desirable concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of protein or its 25 antibodies, antagonists, or inhibitors which ameliorate the symptoms or condition. Therapeutic efficacy and toxicity of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals (*e.g.*, ED<sub>50</sub>, the dose therapeutically effective in 50% of the population; and LD<sub>50</sub>, the dose lethal to 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic 30 index, and it can be expressed as the ratio, LD<sub>50</sub>/ED<sub>50</sub>. Pharmaceutical compositions

which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage is chosen by the individual physician in view of the patient to be treated. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Additional factors which may be taken into account include the severity of the disease state (*e.g.*, tumor size and location); age, weight and gender of the patient; diet; time and frequency of administration; drug combination(s); reaction sensitivities; and tolerance/response to therapy. Long acting pharmaceutical compositions can be administered every 3 to 4 days, every week, or once every two weeks, depending on half-life and clearance rate of the particular formulation. Guidance as to particular dosages and methods of delivery is provided in the literature (*see*, US Patent Nos. 4,657,760; 5,206,344; and 5,225,212; herein incorporated by reference). Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, and the like.

It is contemplated, for example, that human telomerase can be used as a therapeutic molecule to combat disease (*e.g.*, cancer) and/or other problems associated with aging. It is further contemplated that antisense molecules capable of reducing the expression of human telomerase or telomerase protein subunits can be used as therapeutic molecules to treat tumors associated with the aberrant expression of human telomerase. Still further, it is contemplated that antibodies directed against human telomerase and capable of neutralizing the biological activity of human telomerase can be used as therapeutic molecules to treat tumors associated with the aberrant expression of human telomerase and/or telomerase protein subunits.

## DEFINITIONS

To facilitate understanding the invention, a number of terms are defined below.

"Affinity purification" as used herein refers to the purification of ribonucleoprotein particles, through the use of an "affinity oligonucleotide" (*i.e.*, an antisense oligonucleotide) to bind the particle, followed by the step of eluting the particle from the oligonucleotide by means of a "displacement oligonucleotide." In the present invention, the displacement oligonucleotide has a greater degree of complementarity with the affinity oligonucleotide, and therefore produces a more thermodynamically stable duplex than the particle and the affinity oligonucleotide. For example, telomerase may be bound to the affinity oligonucleotide and then eluted by use of a displacement oligonucleotide which binds to the affinity oligonucleotide. In essence, the displacement oligonucleotide displaces the telomerase from the affinity oligonucleotide, allowing the elution of the telomerase. Under sufficiently mild conditions, the method results in the enrichment of functional ribonucleoprotein particles. Thus, the method is useful for the purification of telomerase from a mixture of compounds.

"Alterations in the polynucleotide" as used herein comprise any alteration in the sequence of polynucleotides encoding telomerases, including deletions, insertions, and point mutations, which can be detected using hybridization assays. Included within this definition is the detection of alterations to the genomic DNA sequence which encodes telomerase (*e.g.*, by alterations in pattern of restriction enzyme fragments capable of hybridizing to any sequence such as SEQ ID NOS: 1 or 3 [*e.g.*, RFLP analysis], the inability of a selected fragment of any sequence to hybridize to a sample of genomic DNA [*e.g.*, using allele-specific oligonucleotide probes], improper or unexpected hybridization, such as hybridization to a locus other than the normal chromosomal locus for the telomere or telomerase genes *e.g.*, using FISH to metaphase chromosomes spreads, etc.)).

The term "amino acid sequence" as used herein refers to peptide or protein sequence.

"Amplification" is defined as the production of additional copies of a nucleic acid sequence and is generally carried out using polymerase chain reaction (PCR) or other technologies well known in the art (e.g., Dieffenbach and Dveksler, *PCR Primer, a Laboratory Manual*, Cold Spring Harbor Press, Plainview NY [1995]). As used

5 herein, the term "polymerase chain reaction" ("PCR") refers to the method of K.B. Mullis (U.S. Patent Nos. 4,683,195 and 4,683,202, hereby incorporated by reference), which describe a method for increasing the concentration of a segment of a target sequence in a mixture of genomic DNA without cloning or purification. This process

10 for amplifying the target sequence consists of introducing a large excess of two oligonucleotide primers to the DNA mixture containing the desired target sequence, followed by a precise sequence of thermal cycling in the presence of a DNA polymerase. The two primers are complementary to their respective strands of the double stranded target sequence. To effect amplification, the mixture is denatured and the primers then annealed to their complementary sequences within the target molecule.

15 Following annealing, the primers are extended with a polymerase so as to form a new pair of complementary strands. The steps of denaturation, primer annealing and polymerase extension can be repeated many times (i.e., denaturation, annealing and extension constitute one "cycle"; there can be numerous "cycles") to obtain a high concentration of an amplified segment of the desired target sequence. The length of the

20 amplified segment of the desired target sequence is determined by the relative positions of the primers with respect to each other, and therefore, this length is a controllable parameter. By virtue of the repeating aspect of the process, the method is referred to as the "polymerase chain reaction" (hereinafter "PCR"). Because the desired amplified segments of the target sequence become the predominant sequences (in terms of

25 concentration) in the mixture, they are said to be "PCR amplified".

As used herein, the terms "amplification product" and "PCR product" refer to the resultant mixture of compounds after two or more cycles of the PCR steps of denaturation, annealing and extension are complete. These terms encompass the case where there has been amplification of one or more segments of one or more target

30 sequences. With PCR, it is possible to amplify a single copy of a specific target

sequence in genomic DNA to a level detectable by several different methodologies (e.g., hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme conjugate detection; incorporation of <sup>32</sup>P-labeled deoxynucleotide triphosphates, such as dCTP or dATP, into the amplified segment). In addition to  
5 genomic DNA, any oligonucleotide sequence can be amplified with the appropriate set of primer molecules. In particular, the amplified segments created by the PCR process itself are, themselves, efficient templates for subsequent PCR amplifications.

Amplified target sequences may be used to obtain segments of DNA (e.g., genes) for insertion into recombinant vectors.

10       The term "antibody" refers to a polypeptide substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments or synthetic or recombinant analogues thereof which specifically bind and recognize analytes and antigens. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon and mu constant region genes, as well as myriad  
15 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one  
20 "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V<sub>L</sub>) and variable heavy chain (V<sub>H</sub>) refer to these light and heavy chains respectively. Antibodies exist, e.g., as intact immunoglobulins or as a number of well characterized fragments  
25 produced by digestion with various peptidases, *see*, FUNDAMENTAL IMMUNOLOGY, 3RD ED., W.E. Paul, ed., Raven Press, N.Y. (1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by utilizing recombinant DNA methodologies, for example, recombinant single chain Fv or  
30 antibodies or fragments thereof displayed on the surface of a phage, virus or a cell. The

term immunologically reactive conditions refers to an environment in which antibodies can bind to antigens, such as a TRT of the invention. As discussed below, this can be an immunological binding assay. The phrase "specifically binds to an antibody" when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, antibodies specific for a telomerase TRT protein of this invention or to any portion of a protein defined by a TRT sequence can be selected to immunoreact specifically with all TRT species of the invention or only a single TRT specie of the invention, and not with other non-telomerase proteins. As described below, a variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publications, New York (Harlow and Lane), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity. A specific or selective reaction is one which generates, for example, a signal at least twice (2X) over background signal or "noise."

The term "antigenic determinant" as used herein refers to that portion of an antigen that makes contact with a particular antibody (*i.e.*, an epitope). When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to a given region or three-dimensional structure on the protein; these regions or structures are referred to as antigenic determinants. An antigenic determinant may compete with the intact antigen (*i.e.*, the immunogen used to elicit the immune response) for binding to an antibody.



As used herein, the term "antisense" is used in reference to RNA sequences or other oligonucleotides or nucleic acids, including those containing or composed entirely of synthetic or non-naturally occurring nucleotides or linkages, which are complementary to a specific RNA sequence (*e.g.*, mRNA). Antisense RNA may be produced by any method, including synthesis by splicing the gene(s) of interest in a reverse orientation to a viral promoter which permits the synthesis of a coding strand. Once introduced into a cell, this transcribed strand combines with natural mRNA produced by the cell to form duplexes. These duplexes then block either the further transcription of the mRNA or its translation. In this manner, mutant or altered phenotypes may be generated. The term "antisense strand" is used in reference to a nucleic acid strand that is complementary to the "sense" strand. The designation (-) (*i.e.*, "negative") is sometimes used in reference to the antisense strand, with the designation (+) sometimes used in reference to the sense (*i.e.*, "positive") strand.

The term "biologically active" refers to telomerase (or other) molecules or peptides having structural, regulatory, or biochemical functions of a naturally occurring telomerase (or other) molecule or peptide. Likewise, "immunologically active," defines the capability of the natural, recombinant, or synthetic telomerase proteins or any polypeptide or oligopeptide thereof, to induce a specific immune response in appropriate animals or cells, and to bind with specific antibodies.

As used herein, the term "capable of replicating telomeric DNA" refers to the ability of functional telomerase enzymes to perform the function of replicating DNA located in telomeres. It is contemplated that this term encompass the replication of telomeres, as well as sequences and structures that are commonly found located in telomeric regions of chromosomes. For example, "telomeric DNA" includes, but is not limited to the tandem array of repeat sequences found in the telomeres of most organisms.

As used herein, the term "ciliate" refers to any of the protozoans belonging to the phylum Ciliophora.

As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (*i.e.*, a sequence of nucleotides) related by the base-pairing

rules. For example, for the sequence "5'-A-G-T-3'," is complementary to the sequence "3'-T-C-A-5'." Complementarity may be "partial," in which only some of the nucleotide bases of the double stranded nucleic acid are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods which depend upon binding between nucleic acids.

The term "conservative substitution" refers to a change in the amino acid composition of a protein, such as the TRT of the invention, to a "conservative variant," such that the change(s) do not substantially alter the protein's (the conservative variant's) activity and corresponding changes in nucleotide sequences of nucleic acids. This includes conservatively modified variations of a particular amino acid sequence, *i.e.*, amino acid substitutions of those amino acids that are not critical for protein activity or substitution of amino acids with other amino acids having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter activity. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following six groups each contain amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W) (see also, Creighton (1984) *Proteins*, W.H. Freeman and Company). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations." The term "conservative substitution"

also refers to a change in a nucleic acid sequence to a "conservative variant," such that the substitution does not substantially alter the contemplated activity of the (conservative variant) nucleic acid, for example, as not changing the activity of the protein encoded by the unchanged nucleic acid. A nucleic acid sequence of the invention implicitly encompasses conservative (modified) variants thereof (e.g. degenerate codon substitutions) and complementary sequences and as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer (1991) *Nucleic Acid Res.* 19:5081; Ohtsuka (1985) *J. Biol. Chem.* 260:2605-2608; Rossolini (1994) *Mol. Cell. Probes* 8:91-98).

The term "correlates with expression of a polynucleotide," as used herein, indicates that the detection of the presence of ribonucleic acid (RNA) complementary to a telomerase sequence by hybridization assays is indicative of the presence of mRNA encoding eukaryotic telomerases, including human telomerases in a sample. Such correlation can include expression of the telomerase mRNA from the gene encoding the protein.

A "deletion" is defined as a change in either nucleotide or amino acid sequence in which one or more nucleotides or amino acid residues, respectively, are absent.

The term "derivative" as used herein refers to the chemical structure of a molecule and modifications of such structures, as, for example, a nucleic acid encoding telomerase structures, such as the 123 kDa or 43 kDa protein subunits of the *E. aediculatus* telomerase, or other telomerase proteins or peptides. Illustrative of such modifications would be replacement of hydrogen by an alkyl, acyl, or amino group. A nucleic acid derivative includes a nucleic acid that would encode a polypeptide which retains essential biological characteristics of naturally-occurring telomerase or its subunits.

As used herein, the term "eukaryote" refers to organisms distinguishable from "prokaryotes." It is intended that the term encompass all organisms with cells that exhibit the usual characteristics of eukaryotes such as the presence of a true nucleus

bounded by a nuclear membrane, within which lie the chromosomes, the presence of membrane-bound organelles, and other characteristics commonly observed in eukaryotic organisms. Thus, the term includes, but is not limited to such organisms as fungi, protozoa, and animals (*e.g.*, humans).

5           As used herein, the term "*Euplotes* telomerase polypeptide," refers to a polypeptide which comprises at least a portion of the *Euplotes* telomerase structure. The term encompasses the 123 kDa and 43 kDa polypeptide or protein subunits of the *Euplotes* telomerase. It is also intended that the term encompass variants of these protein subunits. It is further intended to encompass the polypeptides encoded by SEQ  
10 ID NOS: 1 and 3. As molecular weight measurements may vary, depending upon the technique used, it is not intended that the present invention be precisely limited to the 123 kDa or 43 kDa molecular masses of the polypeptides encoded by SEQ ID NOS:1 and 3, as determined by any particular method such as SDS-PAGE.

          The term "expression vector" or "vector" refers to any recombinant expression  
15 system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including a prokaryotic, yeast, fungal, plant, insect or mammalian cell. The expressed nucleic acid sequence is inserted in (spliced into) the vector. The term includes linear or circular nucleic acid expression systems, such as those that remain episomal or integrate into the host cell genome. The  
20 expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression "cassettes" which contain only the minimum elements needed for transcription of a recombinant nucleic acid.

          The terms "homology," "sequence identity" and "sequence similarity" refers to  
25 a degree of complementarity or sequence identity. There may be partial homology or complete homology (*i.e.*, identity). A partially complementary sequence is one that at least partially inhibits a completely complementary sequence from hybridizing to a target nucleic acid and can be referred to using the functional term as "substantially homologous" to the completely complementary sequence. The inhibition of  
30 hybridization of the completely complementary sequence to the target sequence may be

examined using a hybridization assay (Southern or Northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe will compete for and inhibit the binding (*i.e.*, the hybridization) of a completely homologous to a target under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to one another be a specific (*i.e.*, selective) interaction. The absence of non-specific binding may be tested by the use of a second target which lacks even a partial degree of complementarity (*e.g.*, less than about 30% identity); in the complete absence of non-specific binding the probe will not hybridize to the second non-complementary target. The terms "sequence identity," "sequence similarity" and "homology" refer to when two sequences, such as the nucleic acid and amino acid sequences of the hTRT proteins of the telomerase of the invention, when optimally aligned, as with the programs BLAST, GAP, FASTA or BESTFIT, share at least 40 percent to 50 percent sequence identity, and preferably at least 60 percent or greater sequence identity. "Percentage amino acid sequence identity" refers to a comparison of the sequences of two TRT nucleic acids or polypeptides which, when optimally aligned, have approximately the designated percentage of the same nucleotides or amino acids, respectively. For example, "60% sequence identity" and "60% homology" refer to a comparison of the sequences of two nucleic acids or polypeptides which, when optimally aligned, have 60% identity. An additional algorithm that is suitable for determining sequence similarity is the BLAST algorithm, which is described in Altschul (1990) *J. Mol. Biol.* 215: 403-410; Shpaer (1996) *Genomics* 38:179-191. Software for performing BLAST analyses is publicly available at National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al, supra.*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs

containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (*see* Henikoff (1992) *Proc. Natl. Acad. Sci. USA* 89: 10915-10919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands. The term BLAST refers to the BLAST algorithm which performs a statistical analysis of the similarity between two sequences; *see, e.g.,* Karlin (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid can be considered similar to a TRT nucleic acid if the smallest sum probability in a comparison of the test nucleic acid to an TRT nucleic acid is less than about 0.5, 0.2, 0.1, 0.01, or 0.001.

The term "hybridization" as used herein includes "any process by which a strand of nucleic acid joins with a complementary strand through base pairing" (Coombs, *Dictionary of Biotechnology*, Stockton Press, New York NY [1994]. As used herein the term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary G and C bases and between complementary A and T bases; these hydrogen bonds may be further stabilized by base stacking interactions. The two complementary nucleic acid sequences hydrogen bond in an antiparallel configuration. A hybridization complex may be formed in solution (*e.g.,* C<sub>0</sub>t or R<sub>0</sub>t analysis) or between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized to a solid support (*e.g.,* a nylon membrane or a nitrocellulose filter as employed in Southern and

Northern blotting, dot blotting or a glass slide as employed in *in situ* hybridization, including FISH [fluorescent *in situ* hybridization]).

The term "specifically hybridizes" refers to a nucleic acid that hybridizes, duplexes or binds to a particular target DNA or RNA sequence. The target sequences  
5 can be present in a preparation of total cellular DNA or RNA. Proper annealing conditions depend, for example, upon a nucleic acid's, such as a probe's length, base composition, and the number of mismatches and their position on the probe and corresponding target, and can be readily determined empirically providing the appropriate reagents are available. For discussions of nucleic acid probe design and  
10 annealing conditions, see, for example, Sambrook, MOLECULAR CLONING: A LABORATORY MANUAL (2ND ED.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989) (Sambrook), and, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Ausubel, ed. Greene Publishing and Wiley-Interscience, New York (1987) (Ausubel). The terms "stringent hybridization," "stringent hybridization conditions," "stringent conditions," or "specific  
15 hybridization conditions" refer to conditions under which an oligonucleotide (when used, for example, as a probe or primer) will hybridize to its target subsequence, such as a TRT recombinant sequence of a nucleic acid in a biological sample but not to a non-telomerase sequence. Stringent conditions are sequence-dependent. Thus, in one set of stringent conditions an oligonucleotide probe will hybridize to only one specie of  
20 the genus of TRT of the invention. In another set of stringent conditions an oligonucleotide probe will hybridize to all species of the invention's genus of TRT but not to non-telomerase nucleic acids. Longer sequences hybridize specifically at higher temperatures. Stringent conditions are selected to be about 5EC lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$   
25 is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium (if the target sequences are present in excess, at  $T_m$ , 50% of the probes are occupied at equilibrium). Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, *i.e.*, about 0.01 to 1.0  
30 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at

least about 30EC for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60EC for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Often, high stringency wash conditions are preceded by low stringency wash conditions to remove background probe signal. An example of medium stringency wash conditions for a duplex of, *e.g.*, more than 100 nucleotides, is 1x SSC at 45EC for 15 minutes (see Sambrook). An example, low stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 4-6x SSC at 40EC for 15 minutes. A signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a "specific hybridization." Nucleic acids which do not hybridize to each other under stringent conditions can still be substantially identical if the polypeptides which they encode are substantially identical. This can occur, *e.g.*, when a nucleic acid is created that encodes for conservative substitutions. Stringent hybridization and stringent hybridization wash conditions are different under different environmental parameters, such as for Southern and Northern hybridizations. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY-HYBRIDIZATION WITH NUCLEIC ACID PROBES, part I, chapt. 2, Overview of Principles of Hybridization and the Strategy of Nucleic Acid Probe Assays, Elsevier, NY.

An "insertion" or "addition" is that change in a nucleotide or amino acid sequence which has resulted in the addition of one or more nucleotides or amino acid residues, respectively, as compared to, naturally occurring sequences.

As used herein, "isolated," when referring to a molecule or composition, such as, for example, a TRT or a telomerase-associated nucleic acid, means that the molecule or composition is separated from at least one other compound, such as a protein, other nucleic acids (*e.g.*, RNAs), or other contaminants with which it is associated *in vivo* or in its naturally occurring state. Thus, a TRT is considered isolated when the TRT has been isolated from any other component with which it is naturally associated, *e.g.*, cell membrane, as in a cell extract. An isolated composition can, however, also be substantially pure.



The term "label" refers to a detectable composition, such as by spectroscopic, photochemical, biochemical, immunochemical, physical or chemical means. For example, useful labels include  $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ , fluorescent dyes (e.g., FITC, rhodamine, lanthanide phosphors), electron-dense reagents, enzymes, e.g., as  
5 commonly used in an ELISA (e.g., horseradish peroxidase, beta-galactosidase, luciferase, alkaline phosphatase), biotin, dioxigenin, or haptens and proteins for which antisera or monoclonal antibodies are available. The label can be directly incorporated into a nucleic acid, peptide or other target compound to be detected, or it can be attached to a probe or antibody which hybridizes or binds to the target. A peptide can  
10 be made detectable by incorporating predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, transcriptional activator polypeptide, metal binding domains, epitope tags). In some embodiments, labels are attached by spacer arms of various lengths to reduce potential steric hindrance or impact on other useful or desired properties. See for  
15 example, Mansfield (1995) *Mol Cell Probes* 9:145-156.

As used herein, the term "macronucleus" refers to the larger of the two types of nuclei observed in the ciliates. This structure is also sometimes referred to as the "vegetative" nucleus. Macronuclei contain many copies of each gene and are transcriptionally active.

20 As used herein, the term "micronucleus" refers to the smaller of the two types of nuclei observed in the ciliates. This structure is sometimes referred to as the "reproductive" nucleus, as it participates in meiosis and autogamy. Micronuclei are diploid and are transcriptionally inactive.

"Nucleic acid sequence" or "oligonucleotide" as used herein refers to a  
25 deoxyribonucleotide or ribonucleotide oligonucleotide, nucleotide or polynucleotide, and fragments or portions thereof, and to DNA or RNA of natural or synthetic origin which may be single- or double-stranded, or contain a sense or antisense strand. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogues of natural nucleotides which have similar or improved binding or other properties, for the  
30 purposes desired, as the reference nucleic acid. The term also includes nucleic acids

which are metabolized in a manner similar to naturally occurring nucleotides or at rates that are improved thereover for the purposes desired. The term also encompasses nucleic-acid-like structures with synthetic backbones. DNA backbone analogues provided by the invention include phosphodiester, phosphorothioate, 5 phosphorodithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-carbamate, morpholino carbamate, and other nucleic acids; see *Oligonucleotides and Analogues, A Practical Approach*, edited by F. Eckstein, IRL Press at Oxford University Press (1991); *Antisense Strategies*, *Annals of the New York Academy of Sciences*, Volume 600, Eds. 10 Baserga and Denhardt (NYAS 1992); Milligan (1993) *J. Med. Chem.* 36:1923-1937; *Antisense Research and Applications* (1993, CRC Press) in its entirety and specifically Chapter 15, by Sanghvi, entitled "Heterocyclic base modifications in nucleic acids and their applications in antisense oligonucleotides." "Peptide nucleic acid" or "PNA" as used herein refers to an oligomeric molecule in which nucleosides are joined by 15 peptide, rather than phosphodiester, linkages. These small molecules, also designated anti-gene agents, stop transcript elongation by binding to their complementary (template) strand of nucleic acid (Nielsen *et al.*, *Anticancer Drug Des* 8:53-63 [1993]). PNAs contain non-ionic backbones, such as N-(2-aminoethyl) glycine units, as described in USSN 08/630,019, filed 9 April 1996, and the US CIP USSN 08/838,545 20 and PCT application PCT/US/97/05931, both filed on April 9, 1997. Phosphorothioate linkages are described in WO 97/03211; WO 96/39154; Mata (1997) *Toxicol Appl Pharmacol* 144:189-197. Other synthetic backbones encompassed by the term include methylphosphonate linkages or alternating methylphosphonate and phosphodiester linkages (Strauss-Soukup (1997) *Biochemistry* 36:8692-8698), and benzylphosphonate 25 linkages which, compared with unmodified oligonucleotides and methylphosphonates, are more stable against nucleases and exhibit a higher lipophilicity (Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide primer, probe and amplification product. The term "exogenous nucleic acid" refers to a nucleic acid that 30 has been isolated, synthesized, cloned, ligated, excised in conjunction with another

nucleic acid, in a manner that is not found in nature, and/or introduced into and/or expressed in a cell or cellular environment other than or at levels or forms different than the cell or cellular environment in which said nucleic acid or protein is be found in nature. The term encompasses both nucleic acids originally obtained from a different  
5 organism or cell type than the cell type in which it is expressed, and also nucleic acids that are obtained from the same cell line as the cell line in which it is expressed.

As used herein, the term "polymerase" refers to any polymerase suitable for use in the amplification of nucleic acids of interest. It is intended that the term encompass such DNA polymerases as *Taq* DNA polymerase obtained from *Thermus aquaticus*,  
10 although other polymerases, both thermostable and thermolabile are also encompassed by this definition.

As used herein, the term "polyploid" refers to cells or organisms which contain more than two sets of chromosomes.

As used herein the term "portion" when in reference to a protein (as in "a  
15 portion of a given protein") refers to fragments of that protein. The fragments may range in size from four amino acid residues to the entire amino acid sequence minus one amino acid. Thus, a protein "comprising at least a portion of the amino acid sequence of SEQ ID NO:2" encompasses the full-length 123 kDa telomerase protein subunit and fragments thereof.

20 As used herein, the term "probe" refers to a molecule that can specifically bind to another. For example, a probe can be an oligonucleotide (*i.e.*, a sequence of nucleotides), whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of hybridizing to another oligonucleotide or polynucleotide of interest. Probes are useful in the detection, identification and  
25 isolation of particular gene sequences or particular gene products, whether nucleic acid or protein. It is contemplated that any probe used in the present invention can be labelled with any "reporter molecule," that is detectable in any detection system, including, but not limited to enzyme (*e.g.*, ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems. It is further  
30 contemplated that the oligonucleotide, antibody, or other protein or nucleic of interest

(i.e., to be detected) can be labelled with a reporter molecule. It is also contemplated that both the probe and oligonucleotide of interest can be labelled. It is not intended that the present invention be limited to any particular detection system or label.

As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to bacterial or other enzymes, which cut double-stranded or single-stranded DNA at or near a specific nucleotide sequence.

The term "recombinant," when used with reference to a cell or nucleic acid, protein, or vector, refers to a material, or a material corresponding to the natural or native form of the material, that has been modified by the introduction of a new moiety or alteration of an existing moiety, or is identical thereto but produced or derived from synthetic materials. For example, recombinant cells can express genes that are not found within the native (non-recombinant) form of the cell or can express native genes that are otherwise expressed at a different level, typically, under or not expressed. The term "recombinant means" refers to techniques where a recombinant nucleic acid such as a cDNA coding a protein is inserted into an expression vector, the vector is introduced into a cell and the cell expresses the protein. "Recombinant means" also encompass the ligation of nucleic acids having coding or promoter sequences from different sources into one vector for expression of a protein fusion, including proteins such as the TRT proteins of the invention, either constitutively or inducibly.

As used herein, the term "recombinant DNA molecule" refers to a DNA molecule which is comprised of segments of DNA joined together by means of molecular biological techniques and recombinant means.

As used herein, the term "ribonucleoprotein" refers to a complex macromolecule containing both RNA and protein.

The term "sample" as used herein is used in its broadest sense. A biological sample suspected of containing a nucleic acid encoding a telomerase subunit may comprise a cell, chromosomes isolated from a cell (e.g., a spread of metaphase chromosomes), genomic DNA (in solution or bound to a solid support such as for Southern blot analysis), RNA (in solution or bound to a solid support such as for Northern blot analysis), cDNA (in solution or bound to a solid support) and the like. A

sample suspected of containing a protein may comprise a cell, a portion of a tissue, an extract containing one or more proteins and the like.

The terms "specific binding" or "specifically binding" when used in reference to the interaction of an antibody and a protein or peptide means that the interaction is dependent upon the presence of a particular structure (*i.e.*, the antigenic determinant or epitope) on the protein; in other words the antibody is recognizing and binding to a specific protein structure rather than to proteins in general. For example, if an antibody is specific for epitope "A", the presence of a protein containing epitope A (or free, unlabeled A) in a reaction containing labelled "A" and the antibody will reduce the amount of labelled A bound to the antibody.

"Stringency" when used in reference to nucleic acid hybridization or binding typically occurs in a range from about  $T_m - 5\text{EC}$  (5EC below the  $T_m$  of the probe) to about 20EC to 25EC below  $T_m$ . As will be understood by those of skill in the art, a stringent hybridization can be used to identify or detect identical polynucleotide sequences or to identify or detect similar or related polynucleotide sequences. The art knows well that numerous equivalent conditions may be employed to comprise either low or high stringency conditions; factors such as the length and nature (DNA, RNA, base composition) of the probe and nature of the target (DNA, RNA, base composition, present in solution or immobilized, etc.) and the concentration of the salts and other components (*e.g.*, the presence or absence of formamide, dextran sulfate, polyethylene glycol) are considered and the hybridization solution may be varied to generate conditions of either low or high stringency hybridization different from, but equivalent to, the above listed conditions.

A "substitution" results from the replacement of one or more nucleotides or amino acids by different nucleotides or amino acids, respectively.

As used herein, the term " $T_m$ " is used in reference to the "melting temperature." The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. The equation for calculating the  $T_m$  of nucleic acids is well known in the art. As indicated by standard references, a simple estimate of the  $T_m$  value may be calculated by the equation:  $T_m =$

81.5 + 0.41(% G + C), when a nucleic acid is in aqueous solution at 1 M NaCl (*see e.g.*, Anderson and Young, Quantitative Filter Hybridisation, in *Nucleic Acid Hybridisation* (1985). Other references include more sophisticated computations which take structural as well as sequence characteristics into account for the calculation of  $T_m$ .

5           As used herein, the term "target" refers to a molecule to be detected or specifically manipulated. For example, in PCR the target refers to the region of nucleic acid bounded by the primers used for polymerase chain reaction. Thus, the "target" is sought to be sorted out from other nucleic acid sequences. A "segment" is defined as a region of nucleic acid within the target sequence.

10           As used herein, the terms "telomerase" and "telomerase complex" refer to functional telomerase enzymes. It is intended that the terms encompass the complex of proteins and nucleic acids found in telomerases. For example, the terms encompass the 123 kDa and 43 kDa telomerase protein subunits and telomerase RNA of *E. aediculatus*. The terms "TRT" and "telomerase reverse transcriptase" refer to a  
15           telomere-specific RNA-dependent DNA polymerase protein, such as, for example, the 123 kDa telomerase protein subunit of *E. aediculatus*. The terms "TRT" and "telomerase reverse transcriptase" refer to a telomerase holoenzyme without an RNA component, unless indicated otherwise. The term "telomerase" and "telomerase  
20           enzyme" refers to a TRT with an internal RNA component, *i.e.*, an RNA moiety used as a template for DNA synthesis ("TR"). The telomerase can utilize a portion of its internal RNA moiety as a template to specify the addition of telomeric DNA repeat sequences to chromosomal ends. The TRT protein of the invention is a genus of proteins comprising species with common structural characteristics, *i.e.*, motifs, as  
25           discussed in detail below. The TRT of the invention includes species capable of catalyzing the synthesis of telomeres when associated with an RNA moiety (TR), such as hTR, species capable of one or several or all partial activities of telomerase, and species such as TRT isoforms which are considered members of the genus of the invention because they contain requisite common structural characteristics of the genus or sufficient sequence identity with another member of the genus. hTR has been  
30           cloned and characterized, and a variety of useful primers, probes, and expression

vectors have been described, as well as diagnostic and therapeutic methods that target hTR and are useful for diagnosing and treating cancer and other telomerase related diseases, see PCT Publication Nos. 96/01835 and 96/40868 and U.S. Patent No. 5,583,016; see also USSN 08/478,352, 08/472,802 and 08/482,115, all filed 7 June 5 1995; 08/521,634, filed 31 August 1995; 08/714,482, filed 16 September 1996; and 08/770,564 and 08/770,565, both filed 20 December 1996. See also Feng (1995) *Science* 269:1236. In addition, the mouse telomerase RNA component (mTR) has been cloned and characterized, see USSN 08/782,787, filed 10 February 1997; 08/670,516, filed 27 June 1996; and 08/485,778, filed 7 June 1995. hTR knockout mice have been 10 constructed, see USSN 08/623,166, filed 28 March 1996.

The terms "telomerase activity" and "telomerase reverse transcriptase activity" can refer to either "full" or any "partial activity" of a telomerase reverse transcriptase or telomerase. Telomerase reverse transcriptase activity includes the ability to synthesize DNA, such as a telomere or telomeric DNA, using a nucleic acid template, 15 such as the telomerase RNA. A telomerase reverse transcriptase "partial activity" can include, but is not limited to, such functions as the ability of TRT to: bind substrate DNA; to bind the telomerase RNA moiety (TR), *i.e.*, hTR; to catalyze the addition of nucleotides to a DNA substrate; to bind deoxynucleotide substrate; to exhibit "nucleolytic activity" (see Collins (1993) *Genes Dev* 7:1364-1376); to bind telomerase 20 or telomere-associated proteins or chromosomal structures; to exhibit the "processive" or "non-processive" activity of telomerase (see Morin (1989) *Cell* 59:521-529); to exhibit "reverse-transcriptase-like activity" of telomerase (see Lingner (1997) *Science* 276(5312):561-567); to bind nucleotides as part of its enzymatic processive DNA polymerization activity; to bind chromosomes *in vivo*; to bind oligonucleotide primers 25 *in vitro* (Harrington (1995) *J Biol Chem* 270: 8893-8901) or in reconstituted systems; and, to bind histones, nuclear matrix protein, cell division/ cell cycle control proteins and the like.

A "variant" in regard to amino acid sequences indicates an amino acid sequence that differs by one or more amino acids from another, usually related amino acid sequence. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (*e.g.*, replacement of leucine with isoleucine). More rarely, a variant may have "non-conservative" changes, *e.g.*, replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions (*i.e.*, additions), or both. Guidance in determining which and how many amino acid residues may be substituted, inserted or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, DNASTar software. Thus, it is contemplated that this definition will encompass variants of telomerase and/or telomerase protein subunits. For another example, the polypeptides encoded by the three open reading frames (ORFs) of the *Euplotes* 43 kDa polypeptide gene may be considered to be variants of each other, as well as variants of the human homologue of the 43 kDa *Euplotes* gene encoding the polypeptide. Such variants can be tested in functional assays, such as telomerase assays, to detect the presence of functional telomerase in a sample.

## EXPERIMENTAL

The following examples are provided to demonstrate and further illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

In the experimental disclosure which follows, the following abbreviations apply: eq (equivalents); M (Molar);  $\mu$ M (micromolar); N (Normal); mol (moles); mmol (millimoles);  $\mu$ mol (micromoles); nmol (nanomoles); g (grams); mg (milligrams);  $\mu$ g (micrograms); ng (nanograms); l or L (liters); ml (milliliters);  $\mu$ l (microliters); cm (centimeters); mm (millimeters);  $\mu$ m (micrometers); nm (nanometers); EC (degrees Centigrade); RPN (ribonucleoprotein); MeRN (2'-O-methylribonucleotides); dNTP (deoxyribonucleotide); dH<sub>2</sub>O (distilled water); DDT (dithiothreitol); PMSF (phenylmethylsulfonyl fluoride); TE (10 mM Tris HCl, 1 mM EDTA, approximately



pH 7.2); KGlu (potassium glutamate); SSC (salt and sodium citrate buffer); SDS (sodium dodecyl sulfate); PAGE (polyacrylamide gel electrophoresis); Novex (Novex, San Diego, CA); BioRad (Bio-Rad Laboratories, Hercules, CA); Pharmacia (Pharmacia Biotech, Piscataway, NJ); Boehringer-Mannheim (Boehringer-Mannheim Corp.,  
5 Concord, CA); Amersham (Amersham, Inc., Chicago, IL); Stratagene (Stratagene Cloning Systems, La Jolla, CA); NEB (New England Biolabs, Beverly, MA); Pierce (Pierce Chemical Co., Rockford, IL); Beckman (Beckman Instruments, Fullerton, CA); Lab Industries (Lab Industries, Inc., Berkeley, CA); Eppendorf (Eppendorf Scientific, Madison, WI); and Molecular Dynamics (Molecular Dynamics, Sunnyvale, CA).

10

**EXAMPLE 1: Growth of *Euplotes aediculatus***

In this Example, cultures of *E. aediculatus* were obtained from Dr. David Prescott, MCDB, University of Colorado. Dr. Prescott originally isolated this culture from pond water, although this organism is also available from the ATCC (ATCC  
15 #30859). Cultures were grown as described (Swanton (1980) *Chromosoma* 77:203), under non-sterile conditions, in 15-liter glass containers containing *Chlorogonium* as a food source. Organisms were harvested from the cultures when the density reached approximately  $10^4$  cells/ml.

20 **EXAMPLE 2: Preparation of Nuclear Extracts**

In this Example, nuclear extracts of *E. aediculatus* were prepared as described in the art (Lingner (1994) *Genes Develop.* 8:1984), with minor modifications, as indicated below. Briefly, cells grown as described in Example 1 were concentrated with 15  $\mu$ m Nytex filters and cooled on ice. The cell pellet was resuspended in a final  
25 volume of 110 ml TMS/PMSF/spermidine phosphate buffer. The stock TMS/ PMSF/ spermidine phosphate buffer was prepared by adding 0.075 g spermidine phosphate (USB) and 0.75 ml PMSF (from 100 mM stock prepared in ethanol) to 150 ml TMS. TMS comprised 10 mM Tris-acetate, 10 mM  $MgCl_2$ , 85.5752 g sucrose/liter, and 0.33297 g  $CaCl_2$ /liter, pH 7.5.

After resuspension in TMS/PMSF/spermidine phosphate buffer, 8.8 ml 10% NP-40 and 94.1 g sucrose were added and the mixture placed in a siliconized glass beaker with a stainless steel stirring rod attached to an overhead motor. The mixture was stirred until the cells were completely lysed (approximately 20 minutes). The mixture was then centrifuged for 10 minutes at 7500 rpm (8950 x g), at 4EC, using a Beckman JS-13 swing-out rotor. The supernatant was removed and nuclei pellet was resuspended in TMS/PMSF/spermidine phosphate buffer, and centrifuged again, for 5 minutes at 7500 rpm (8950 x g), at 4EC, using a Beckman JS-13 swing-out rotor.

The supernatant was removed and the nuclei pellet was resuspended in a buffer comprised of 50 mM Tris-acetate, 10 mM MgCl<sub>2</sub>, 10% glycerol, 0.1% NP-40, 0.4 M KGlu, 0.5 mM PMSF, pH 7.5, at a volume of 0.5 ml buffer per 10 g of harvested cells. The resuspended nuclei were then dounced in a glass homogenizer with approximately 50 strokes, and then centrifuged for 25 minutes at 14,000 rpm at 4EC, in an Eppendorf centrifuge. The supernatant containing the nuclear extract was collected, frozen in liquid nitrogen, and stored at -80EC until used.

### **EXAMPLE 3: Purification of Telomerase**

In this Example, nuclear extracts prepared as described in Example 2 were used to purify *E. aediculatus* telomerase. In this purification protocol, telomerase was first enriched by chromatography on an Affi-Gel-heparin column, and then extensively purified by affinity purification with an antisense oligonucleotide. As the template region of telomerase RNA is accessible to hybridization in the telomerase RNP particle, an antisense oligonucleotide (*i.e.*, the "affinity oligonucleotide") was synthesized that was complementary to this template region as an affinity bait for the telomerase. A biotin residue was included at the 5' end of the oligonucleotide to immobilize it to an avidin column.

Following the binding of the telomerase to the oligonucleotide, and extensive washing, the telomerase was eluted by use of a displacement oligonucleotide. The affinity oligonucleotide included DNA bases that were not complementary to the telomerase RNA 5' to the telomerase-specific sequence. As the displacement

oligonucleotide was complementary to the affinity oligonucleotide for its entire length, it was able to form a more thermodynamically stable duplex than the telomerase bound to the affinity oligonucleotide. Thus, addition of the displacement oligonucleotide resulted in the elution of the telomerase from the column.

5           The nuclear extracts prepared from 45 liter cultures were frozen until a total of 34 ml of nuclear extract was collected. This corresponded to 630 liters of culture (*i.e.*, approximately  $4 \times 10^9$  cells). The nuclear extract was diluted with a buffer to 410 ml, to provide final concentrations of 20 mM Tris-acetate, 1 mM  $MgCl_2$ , 0.1 mM EDTA, 33 mM KGlu, 10% (vol/vol) glycerol, 1 mM dithiothreitol (DTT), and 0.5 mM  
10       phenylmethylsulfonyl fluoride (PMSF), at a pH of 7.5.

          The diluted nuclear extract was applied to an Affi-Gel-heparin gel column (Bio-Rad), with a 230 ml bed volume and 5 cm diameter, equilibrated in the same buffer and eluted with a 2-liter gradient from 33 to 450 mM KGlu. The column was run at 4EC, at a flow rate of 1 column volume/hour. Fractions of 50 mls each were collected and  
15       assayed for telomerase activity as described in Example 4. Telomerase was eluted from the column at approximately 170 mM KGlu. Fractions containing telomerase (approximately 440 ml) were pooled and adjusted to 20 mM Tris-acetate, 10 mM  $MgCl_2$ , 1 mM EDTA, 300 mM KGlu, 10% glycerol, 1 mM DTT, and 1% Nonidet P-40. This buffer was designated as "WB."

20           To this preparation, 1.5 nmol of each of two competitor DNA oligonucleotides (5'-TAGACCTGTTAGTGTACATTTGAATTGAAGC-3' (SEQ ID NO:28)) and (5'-TAGACCTGTTAGGTTGGATTTGTGGCATCA-3' (SEQ ID NO:29)), 50  $\mu$ g yeast RNA (Sigma), and 0.3 nmol of biotin-labelled telomerase-specific oligonucleotide (5'-biotin-TAGACCTGTTA-(MeRN G)<sub>2</sub>-(MeRN U)<sub>4</sub>-(MeRN G)<sub>4</sub>-(MeRN U)<sub>4</sub>-MeRN G-  
25       3') (SEQ ID NO:60), were added per ml of the pool. The 2-*O*-methyribonucleotides of the telomerase specific oligonucleotides were complementary to the telomerase RNA template region; the deoxyribonucleotides were not complementary. The inclusion of competitor, non-specific DNA oligonucleotides increased the efficiency of the purification, as the effects of nucleic acid binding proteins and other components in the

mixture that would either bind to the affinity oligonucleotide or remove the telomerase from the mixture were minimized.

This material was then added to Ultralink immobilized neutravidin plus (Pierce) column material, at a volume of 60  $\mu$ l of suspension per ml of pool. The column material was pre-blocked twice for 15 minutes each blocking, with a preparation of WB  
5 containing 0.01% Nonidet P-40, 0.5 mg BSA, 0.5 mg/ml lysozyme, 0.05 mg/ml glycogen, and 0.1 mg/ml yeast RNA. The blocking was conducted at 4EC, using a rotating wheel to block the column material thoroughly. After the first blocking step, and before the second blocking step, the column material was centrifuged at 200 x g for  
10 2 minutes to pellet the matrix.

The pool-column mixture was incubated for 8 minutes at 30EC, and then for an additional 2 hours at 4EC, on a rotating wheel (approximately 10 rpm; Labindustries) to allow binding. The pool-column mixture was then centrifuged 200 xg for 2 minutes, and the supernatant containing unbound material was removed. The pool-column  
15 mixture was then washed. This washing process included the steps of rinsing the pool-column mixture with WB at 4EC, washing the mixture for 15 minutes with WB at 4EC, rinsing with WB, washing for 5 minutes at 30EC, with WB containing 0.6 M KGlu, and no Nonidet P-40, washing 5 minutes at 25EC with WB, and finally, rinsing again with WB. The volume remaining after the final wash was kept small, in order to yield a  
20 ratio of buffer to column material of approximately 1:1.

Telomerase was eluted from the column material by adding 1 nmol of displacement deoxyoligonucleotide (5'-CA<sub>4</sub>C<sub>4</sub>A<sub>4</sub>C<sub>2</sub>TA<sub>2</sub>CAG<sub>2</sub>TCTA-3')(SEQ ID NO:30), per ml of column material and incubating at 25EC for 30 minutes. The material was centrifuged for 2 minutes at 14,000 rpm in a microcentrifuge (Eppendorf),  
25 and the eluate collected. The elution procedure was repeated twice more, using fresh displacement oligonucleotide each time. As mentioned above, because the displacement oligonucleotide was complementary to the affinity oligonucleotide, it formed a more thermodynamically stable complex with the affinity oligonucleotide than the telomerase. Thus, addition of the displacement oligonucleotide to an affinity-  
30 bound telomerase resulted in efficient elution of telomerase under native conditions.

The telomerase appeared to be approximately 50% pure at this stage, as judged by analysis on a protein gel. The affinity purification of telomerase and elution with a displacement oligonucleotide is shown in Figure 1 (panels A and B, respectively). In this Figure, the 2'-O-methyl sugars of the affinity oligonucleotide are indicated by the bold line. The black and shaded oval shapes in this Figure are intended to represent the protein subunits of the present invention graphically.

The protein concentrations of the extract and material obtained following Affi-Gel-heparin column chromatography were determined using the method of Bradford (Bradford (1976) *Anal. Biochem.* 72:248), using BSA as the standard. Only a fraction of the telomerase preparation was further purified on a glycerol gradient.

The sedimentation coefficient of telomerase was determined by glycerol gradient centrifugation, as described in Example 8.

Table 1 below is a purification table for telomerase purified according to the methods of this Example. The telomerase was enriched 12-fold in nuclear extracts, as compared to whole cell extracts, with a recovery of 80%; 85% of telomerase was solubilized from nuclei upon extraction.

**Table 1. Purification of Telomerase**

Fraction	Protein (mg)	Telomerase (pmol of RNP)	Telomerase/Protein/pmol of RNP/mg	Recovery (%)	Purification Factor
Nuclear Extract	2020	1720	0.9	100	1
Heparin	125	1040	8.3	60	10
Affinity	0.3**	680	2270	40	2670
Glycerol Gradient	NA*	NA*	NA*	25	NA*

\*NA=Not available

\*\*This value was calculated from the measured amount of telomerase (680 pmol), by assuming a purity of 50% (based on a protein gel).

**EXAMPLE 4: Telomerase Activity**

At each step in the purification of telomerase, the preparation was analyzed by three separate assays, one of which was activity, as described in this Example. In general, telomerase assays were done in 40  $\mu$ l containing 0.003-0.3  $\mu$ l of nuclear extract, 50 mM Tris-Cl (pH 7.5), 50 mM KGlu, 10 mM  $MgCl_2$ , 1 mM DTT, 125  $\mu$ M dTTP, 125  $\mu$ M dGTP, and approximately 0.2 pmoles of 5'- $^{32}P$ -labelled oligonucleotide substrate (*i.e.*, approximately 400,000 cpm). Oligonucleotide primers were heat-denatured prior to their addition to the reaction mixture. Reactions were assembled on ice and incubated for 30 minutes at 25EC. The reactions were stopped by addition of 200  $\mu$ l of 10 mM Tris-Cl (pH 7.5), 15 mM EDTA, 0.6% SDS, and 0.05 mg/ml proteinase K, and incubated for at least 30 minutes at 45EC. After ethanol precipitation, the products were analyzed on denaturing 8% PAGE gels, as known in the art (*See e.g.*, Sambrook *et al.*, 1989).

**EXAMPLE 5: Quantitation of Telomerase Activity**

In this Example, quantitation of telomerase activity through the purification procedure is described. Quantitation was accomplished by assaying the elongation of oligonucleotide primers in the presence of dGTP and [ $\gamma$ - $^{32}P$ ]dTTP. Briefly, 1  $\mu$ M 5'-(G<sub>4</sub>T<sub>4</sub>)<sub>2</sub>-3' oligonucleotide was extended in a 20  $\mu$ l reaction mixture in the presence of 2  $\mu$ l of [ $\gamma$ - $^{32}P$ ]dTTP (10 mCi/ml, 400 Ci/mmol; 1 Ci=37 GBq), and 125  $\mu$ M dGTP as described (Lingner *et al.*, Genes Develop., 8:1984 [1994]), and loaded onto an 8% PAGE sequencing gel as is known in the art.

The results of this study are shown in Figure 3. In lane 1, there is no telomerase present (*i.e.*, a negative control); lanes 2, 5, 8, and 11 contained 0.14 fmol telomerase; lanes 3, 6, 9, and 12 contained 0.42 fmol telomerase; and lanes 4, 7, 10, and 13 contained 1.3 fmol telomerase. Activity was quantified using a PhosphorImager (Molecular Dynamics) using the manufacturer's instructions. It was determined that under these conditions, 1 fmol of affinity-purified telomerase incorporated 21 fmol of dTTP in 30 minutes.

As shown in this Figure 3, the specific activity of the telomerase did not change significantly through the purification procedure. Affinity-purified telomerase was fully active. However, it was determined that at high concentrations, an inhibitory activity was detected and the activity of crude extracts was not linear. Thus, in the assay shown in Figure 3, the crude extract was diluted 700-7000-fold. Upon purification, this inhibitory activity was removed and no inhibitory effect was detected in the purified telomerase preparations, even at high enzyme concentrations.

#### **EXAMPLE 6: Gel Electrophoresis and Northern Blots**

As indicated in Example 4, at each step in the purification of telomerase, the preparation was analyzed by three separate assays. This Example describes the gel electrophoresis and blotting procedures used to quantify telomerase RNA present in fractions and analyze the integrity of the telomerase ribonucleoprotein particle.

#### **Denaturing Gels and Northern Blots**

In this Example, synthetic T7-transcribed telomerase RNA of known concentration served as the standard. Throughout this investigation, the RNA component was used as a measure of telomerase.

A construct for phage T7 RNA polymerase transcription of *E. aediculatus* telomerase RNA was produced using PCR. The telomerase RNA gene was amplified with primers that annealed to either end of the gene. The primer that annealed at the 5' end also encoded a hammerhead ribozyme sequence to generate the natural 5' end upon cleavage of the transcribed RNA, a T7-promoter sequence, and an *EcoRI* site for subcloning. The sequence of this 5' primer was 5'-

GCGGGAATTCTAATACGACTCACTATAGGGAAGAACTCTGATGAGGCCGA  
AAGGCCGAACTCCACGAAAGTGGAGTAAGTTTCTCGATAATTGATCTGTA  
G-3' (SEQ ID NO:31). The 3' primer included an *EaeI* site for termination of transcription at the natural 3' end, and a *BamHI* site for cloning. The sequence of this 3' primer was 5'-CGGGGATCCTCTTCAAAAGATGAGAGGACAGCAAAC-3' (SEQ ID NO:32). The PCR amplification product was cleaved with *EcoRI* and *BamHI*, and

subcloned into the respective sites of pUC19 (NEB), to give "pEaT7." The correctness of this insert was confirmed by DNA sequencing. T7 transcription was performed as described by Zaug *Biochemistry* (1994) 33:14935, with *EaeI*-linearized plasmid. RNA was gel-purified and the concentration was determined (an  $A_{260}$  of 1 = 40  $\mu\text{g/ml}$ ). This  
5 RNA was used as a standard to determine the telomerase RNA present in various preparations of telomerase.

The signal of hybridization was proportional to the amount of telomerase RNA, and the derived RNA concentrations were consistent with, but slightly higher than those obtained by native gel electrophoresis. Comparison of the amount of whole telomerase  
10 RNA in whole cell RNA to serial dilutions of known T7 RNA transcript concentrations indicated that each *E. aediculatus* cell contained approximately 300,000 telomerase molecules.

Visualization of the telomerase was accomplished by Northern blot hybridization to its RNA component, using the methods described (Linger (1994)  
15 *Genes Develop.* 8:1984). Briefly, RNA (less than or equal to 0.5  $\mu\text{g/lane}$ ) was resolved on an 8% PAGE and electroblotted onto a Hybond-N membrane (Amersham), as known in the art (*see e.g.*, Sambrook *et al.*, 1989). The blot was hybridized overnight in 10 ml of 4x SSC, 10x Denhardt's solution, 0.1% SDS, and 50  $\mu\text{g/ml}$  denatured herring sperm DNA. After pre-hybridizing for 3 hours,  $2 \times 10^6$  cpm probe/ml  
20 hybridization solution was added. The randomly labelled probe was a PCR-product that covered the entire telomerase RNA gene. The blot was washed with several buffer changes for 30 minutes in 2x SSC, 0.1% SDS, and then washed for 1 hour in 0.1x SSC and 0.1% SDS at 45EC.

## 25 Native Gels and Northern Blots

In this experiment, the purified telomerase preparation was run on native (*i.e.*, non-denaturing) gels of 3.5% polyacrylamide and 0.33% agarose, as known in the art and described (Lamond (1994), *supra*). The telomerase comigrated approximately with the xylene cyanol dye.



The native gel results indicated that telomerase was maintained as an RNP throughout the purification protocol. Figure 2 is a photograph of a Northern blot showing the mobility of the telomerase in different fractions on a non-denaturing gel as well as *in vitro* transcribed telomerase. In this figure, lane 1 contained 1.5 fmol telomerase RNA, lane 2 contained 4.6 fmol telomerase RNA, lane 3 contained 14 fmol telomerase RNA, lane 4 contained 41 fmol telomerase RNA, lane 5 contained nuclear extract (42 fmol telomerase), lane 6 contained Affi-Gel-heparin-purified telomerase (47 fmol telomerase), lane 7 contained affinity-purified telomerase (68 fmol), and lane 8 contained glycerol gradient-purified telomerase (35 fmol).

As shown in Figure 2, in nuclear extracts, the telomerase was assembled into an RNP particle that migrated slower than unassembled telomerase RNA. Less than 1% free RNA was detected by this method. However, a slower migrating telomerase RNP complex was also sometimes detected in extracts. Upon purification on the Affi-Gel-heparin column, the telomerase RNP particle did not change in mobility (Figure 2, lane 6). However, upon affinity purification the mobility of the RNA particle slightly increased (Figure 2, lane 7), perhaps indicating that a protein subunit or fragment had been lost. On glycerol gradients, the affinity-purified telomerase did not change in size, but approximately 2% free telomerase RNA was detectable (Figure 2, lane 8), suggesting that a small amount of disassembly of the RNP particle had occurred.

#### **EXAMPLE 7: Telomerase Protein Composition**

In this Example, the analysis of the purified telomerase protein composition are described. Glycerol gradient fractions obtained as described in Example 8, were separated on a 4-20% polyacrylamide gel (Novex). Following electrophoresis, the gel was stained with Coomassie brilliant blue. Figure 4 shows a photograph of the gel. Lanes 1 and 2 contained molecular mass markers (Pharmacia) as indicated on the left side of the gel shown in Figure 4. Lanes 3-5 contained glycerol gradient fraction pools as indicated on the top of the gel (*i.e.*, lane 3 contained fractions 9-14, lane 4 contained fractions 15-22, and lane 5 contained fractions 23-32). Lane 4 contained the pool with 1 pmol of telomerase RNA. In lanes 6-9 BSA standards were run at concentrations

indicated at the top of the gel in Figure 4 (*i.e.*, lane 6 contained 0.5 pmol BSA, lane 7 contained 1.5 pmol BSA, lane 8 contained 4.5 BSA, and lane 9 contained 15 pmol BSA).

As shown in Figure 4, polypeptides with molecular masses of 120 and 43 kDa co-purified with the telomerase. The 43 kDa polypeptide was observed as a doublet. It was noted that the polypeptide of approximately 43 kDa in lane 3 migrated differently than the doublet in lane 4; it may be an unrelated protein. The 120 kDa and 43 kDa doublet each stained with Coomassie brilliant blue at approximately the level of 1 pmol, when compared with BSA standards. Because this fraction contained 1 pmol of telomerase RNA, all of which was assembled into an RNP particle (*See*, Figure 2, lane 8), there appear to be two polypeptide subunits that are stoichiometric with the telomerase RNA. However, it is also possible that the two proteins around 43 kDa are separate enzyme subunits.

Affinity-purified telomerase that was not subjected to fractionation on a glycerol gradient contained additional polypeptides with apparent molecular masses of 35 and 37 kDa, respectively. This latter fraction was estimated to be at least 50% pure. However, the 35 kDa and 37 kDa polypeptides that were present in the affinity-purified material were not reproducibly separated by glycerol gradient centrifugation. These polypeptides may be contaminants, as they were not visible in all activity-containing preparations.

#### **EXAMPLE 8: Sedimentation Coefficient**

The sedimentation coefficient for telomerase was determined by glycerol gradient centrifugation. In this Example, nuclear extract and affinity-purified telomerase were fractionated on 15-40% glycerol gradients containing 20 mM Tris-acetate, with 1 mM MgCl<sub>2</sub>, 0.1 mM EDTA, 300 mM KGlu, and 1 mM DTT, at pH 7.5. Glycerol gradients were poured in 5 ml (13 x 51 mm) tubes, and centrifuged using an SW55Ti rotor (Beckman) at 55,000 rpm for 14 hours at 4°C.

Marker proteins were run in a parallel gradient and had a sedimentation coefficient of 7.6 S for alcohol dehydrogenase (ADH), 113 S for catalase, 17.3 S for

apoferritin, and 19.3 S for thyroglobulin. The telomerase peak was identified by native gel electrophoresis of gradient fractions followed by blot hybridization to its RNA component.

Figure 5 is a graph showing the sedimentation coefficient for telomerase. As shown in this Figure, affinity-purified telomerase co-sedimented with catalase at 11.5 S, while telomerase in nuclear extracts sedimented slightly faster, peaking around 12.5 S. Therefore, consistent with the mobility of the enzyme in native gels, purified telomerase appears to have lost a proteolytic fragment or a loosely associated subunit.

The calculated molecular mass for telomerase, if it is assumed to consist of one 120 kDa protein subunit, one 43 kDa subunit, and one RNA subunit of 66 kDa, adds up to a total of 229 kDa. This is in close agreement with the 232 kDa molecular mass of catalase. However, the sedimentation coefficient is a function of the molecular mass, as well as the partial specific volume and the frictional coefficient of the molecule, both of which are unknown for the *Euplotes* telomerase RNP.

#### **EXAMPLE 9: Substrate Utilization**

In this Example, the substrate requirements of *Euplotes* telomerase were investigated. One simple model for DNA end replication predicts that after semi-conservative DNA replication, telomerase extends double-stranded, blunt-ended DNA molecules. In a variation of this model, a single-stranded 3' end is created by a helicase or nuclease after replication. This 3' end is then used by telomerase for binding and extension.

To determine whether telomerase is capable of elongating blunt-ended molecules, model hairpins were synthesized with telomeric repeats positioned at their 3' ends. These primer substrates were gel-purified, 5'-end labelled with polynucleotide kinase, heated at 0.4  $\mu$ M to 80EC for 5 minutes, and then slowly cooled to room temperature in a heating block, to allow renaturation and helix formation of the hairpins. Substrate mobility on a non-denaturing gel indicated that very efficient hairpin formation was present, as compared to dimerization.

Assays were performed with unlabelled 125  $\mu$ M dGTP, 125  $\mu$ M dTTP, and 0.02  $\mu$ M 5'-end-labelled primer (5'-<sup>32</sup>P-labelled oligonucleotide substrate) in 10  $\mu$ l reaction mixtures that contained 20 mM Tris-acetate, with 10 mM MgCl<sub>2</sub>, 50 mM KGlu, and 1 mM DTT, at pH 7.5. These mixtures were incubated at 25°C for 30 minutes.

- 5 Reactions were stopped by adding formamide loading buffer (*i.e.*, TBE, formamide, bromthymol blue, and cyanol, Sambrook, 1989, *supra*).

Primers were incubated without telomerase ("-"), with 5.9 fmol of affinity-purified telomerase ("+"), or with 17.6 fmol of affinity-purified telomerase ("+++"). Affinity-purified telomerase used in this assay was dialyzed with a membrane having a  
 10 molecular cut-off of 100 kDa, in order to remove the displacement oligonucleotide. Reaction products were separated on an 8% PAGE/urea gel containing 36% formamide, to denature the hairpins. The sequences of the primers used in this study, as well as their lane assignments are shown in Table 2.

**TABLE 2. Primer Sequences**

15	<b>Lane</b>	<b>Primer Sequence (5' to 3')</b>	<b>SEQ ID NO:</b>
	1-3	C <sub>4</sub> (A <sub>4</sub> C <sub>4</sub> ) <sub>3</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub> G <sub>4</sub>	SEQ ID NO:33
	4-6	C <sub>2</sub> (A <sub>4</sub> C <sub>4</sub> ) <sub>3</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub> G <sub>4</sub>	SEQ ID NO:34
	7-9	(A <sub>4</sub> C <sub>4</sub> ) <sub>3</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub> G <sub>4</sub>	SEQ ID NO:35
	10-12	A <sub>2</sub> C <sub>4</sub> (A <sub>4</sub> C <sub>4</sub> ) <sub>2</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub> G <sub>4</sub>	SEQ ID NO:36
20	13-15	C <sub>4</sub> (A <sub>4</sub> C <sub>4</sub> ) <sub>2</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub>	SEQ ID NO:37
	16-18	(A <sub>4</sub> C <sub>4</sub> ) <sub>3</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub>	SEQ ID NO:38
	19-21	A <sub>2</sub> C <sub>4</sub> (A <sub>4</sub> C <sub>4</sub> ) <sub>2</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub>	SEQ ID NO:39
	22-24	C <sub>4</sub> (A <sub>4</sub> C <sub>4</sub> ) <sub>2</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub>	SEQ ID NO:40
	25-27	C <sub>2</sub> (A <sub>4</sub> C <sub>4</sub> ) <sub>2</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub>	SEQ ID NO:41
25	28-30	(A <sub>4</sub> C <sub>4</sub> ) <sub>2</sub> CACA(G <sub>4</sub> T <sub>4</sub> ) <sub>3</sub>	SEQ ID NO:42

The gel results are shown in Figure 6. Lanes 1-15 contained substrates with telomeric repeats ending with four G residues. Lanes 16-30 contained substrates with telomeric repeats ending with four T residues. The putative alignment on the  
 30 telomerase RNA template is indicated in Figure 7 (SEQ ID NOS:43 and 44, and 45 and

46, respectively). It was assumed that the primer sets anneal at two very different positions in the template shown in Figure 7 (*i.e.*, panel A and B, respectively). This may have affected their binding and/or elongation rate.

Figure 8 shows a lighter exposure of lanes 25-30 in Figure 6. The lighter exposure of Figure 8 was taken to permit visualization of the nucleotides that are added and the positions of pausing in elongated products. Percent of substrate elongated for the third lane in each set was quantified on a PhosphorImager, as indicated on the bottom of Figure 6.

The substrate efficiencies for these hairpins were compared with double-stranded telomere-like substrates with overhangs of differing lengths. A model substrate that ended with four G residues (see lanes 1 to 15 of Figure 6) was not elongated when it was blunt ended (see lanes 1-3). However, slight extension was observed with an overhang length of two bases; elongation became efficient when the overhang was at least 4 bases in length. The telomerase acted in a similar manner with a double-stranded substrate that ended with four T residues, with a 6-base overhang required for highly efficient elongation. In Figure 6, the faint bands below the primers in lanes 10-15 that are independent of telomerase represent shorter oligonucleotides in the primer preparations.

The lighter exposure of lanes 25-30 in Figure 8 shows a ladder of elongated products, with the darkest bands correlating with the putative 5' boundary of the template (as described by Lingner *et al.*, Genes Develop., 8:1984 [1994]). The abundance of products that correspond to other positions in the template suggested that pausing and/or dissociation occurs at sites other than the site of translocation with the purified telomerase.

As shown in Figure 6, double-stranded, blunt-ended oligonucleotides were not substrates for telomerase. To determine whether these molecules would bind to telomerase, a competition experiment was performed. In this experiment, 2 nM of 5'-end labelled substrate with the sequence (G<sub>4</sub>T<sub>4</sub>)<sub>2</sub> (SEQ ID NO:61), or a hairpin substrate with a six base overhang were extended with 0.125 nM telomerase (Figure 6, lanes 25-27). Although the same unlabeled oligonucleotide substrates competed efficiently with

labelled substrate for extension, no reduction of activity was observed when the double-stranded blunt-ended hairpin oligonucleotides were used as competitors, even in the presence of 100-fold excess hairpins.

These results indicated that double-stranded, blunt-ended oligonucleotides cannot bind to telomerase at the concentrations and conditions tested in this Example. Rather, a single-stranded 3' end is required for binding. It is likely that this 3' end is required to base pair with the telomerase RNA template.

#### **EXAMPLE 10: Cloning & Sequencing of the 123 kDa Polypeptide**

In this Example, the cloning of the *Euplotes* 123 kDa polypeptide of telomerase (*i.e.*, the 123 kDa protein subunit) is described. In this study, an internal fragment of the telomerase gene was amplified by PCR, with oligonucleotide primers designed to match peptide sequences that were obtained from the purified polypeptide obtained in Example 3, above. The polypeptide sequence was determined using the nanoES tandem mass spectroscopy methods known in the art and described by Calvio (1995) RNA 1:724-733. The oligonucleotide primers used in this Example had the following sequences, with positions that were degenerate shown in parentheses: 5'-TCT(G/A)AA(G/A)TA(G/A)TG(T/G/A)GT(G/A/T/C)A(T/G/A)(G/A)TT(G/A)TTCAT-3' (SEQ ID NO:47), and 5'-GCGGATCCATGAA (T/C)CC(A/T)GA(G/A)AA(T/C)CC(A/T)AA(T/C)GT-3' (SEQ ID NO:48).

A 50 µl reaction contained 0.2 mM dNTPs, 0.15 µg *E. aediculatus* chromosomal DNA, 0.5 µl *Taq* (Boehringer-Mannheim), 0.8 µg of each primer, and 1x reaction buffer (Boehringer-Mannheim). The reaction was incubated in a thermocycler (Perkin-Elmer), using the following--5 minutes at 95EC, followed by 30 cycles of 1 minute at 94EC, 1 minute at 52EC, and 2 minutes at 72EC. The reaction was completed by a 10 minute incubation at 72EC.

A genomic DNA library was prepared from the chromosomal *E. aediculatus* DNA by cloning blunt-ended DNA into the *Sma*I site of pCR-Script plasmid vector (Stratagene). This library was screened by colony hybridization, with the radiolabelled, gel-purified PCR product. Plasmid DNA of positive clones was prepared and

sequenced by the dideoxy method (Sanger *et al.*, Proc. Natl. Acad. Sci., 74:5463 [1977]) or manually, through use of an automated sequencer (ABI). The DNA sequence of the gene encoding this polypeptide is shown in Figure 9 (SEQ ID NO:1). The start codon in this sequence inferred from the DNA sequence, is located at nucleotide position 101, and the open reading frame ends at position 3193. The genetic code of *Euplotes* differs from other organisms in that the "UGA" codon encodes a cysteine residue. The amino acid sequence of the polypeptide inferred from the DNA sequence is shown in Figure 10 (SEQ ID NO:2), and assumes that no unusual amino acids are inserted during translation and no post-translational modification occurs.

#### **EXAMPLE 11: Cloning & Sequencing of the 43 kDa Polypeptide**

The invention provides for isoforms and homologues of the *Euplotes* p43 (43 kDa) telomerase, including the human p43 (kDa) homologue. Such 43 kDa nucleic acids and corresponding proteins, as members of the telomerase subunit genus, can also be identified and isolated using the reagents provided by the invention and the methods described herein. The identification and cloning of the *Euplotes* 43 kDa polypeptide, described below, provides an illustrative example of a means to isolate further members of the 43 kDa sub-genus.

In this Example, the cloning of the 43 kDa polypeptide of *Euplotes* telomerase (*i.e.*, the 43 kDa protein subunit) is described. In this study, an internal fragment of the corresponding telomerase gene was amplified by PCR, with oligonucleotide primers designed to match peptide sequences that were obtained from the purified polypeptide obtained in Example 3, above. The polypeptide sequence was determined using the nanoES tandem mass spectroscopy methods known in the art and described by Calvio, *supra*). The oligonucleotide primers used in this Example had the following sequences- 5'-NNNGTNAC(C/T/A)GG(C/T/A)AT(C/T/A)AA(C/T)AA-3' (SEQ ID NO:49), and 5'-(T/G/A)GC(T/G/A)GT(C/T)TC(T/C)TG(G/A)TC(G/A)TT(G/A)TA-3' (SEQ ID NO:50). In this sequence, "N" indicates the presence of any of the four nucleotides (*i.e.*, A, T, G, or C).

The PCR was performed as described above in Example 10. A genomic DNA library was prepared and sequenced as described above in Example 10. The DNA sequence of the gene encoding this polypeptide is shown in Figure 11 (SEQ ID NO:3). Three potential reading frames are shown for this sequence, as shown in Figure 12.

5 For clarity, the amino acid sequence is indicated below the nucleotide sequence in all three reading frames. These reading frames are designated as "a," "b," and "c," also as shown in SEQ ID NOS:4, 5, and 6, respectively. A possible start codon is encoded at nucleotide position 84 in reading frame "c." The coding region could end at position 1501 in reading frame "b." Early stop codons, indicated by asterisks in this figure,  
10 occur in all three reading frames between nucleotide position 337-350.

The "La-domain" is indicated in bold-face type. Further downstream, the protein sequence appears to be encoded by different reading frames, as none of the three frames is uninterrupted by stop codons. Furthermore, peptide sequences from purified protein are encoded in all three frames. Therefore, this gene appears to contain  
15 intervening sequences, or in the alternative, the RNA is edited. Other possibilities include ribosomal frame-shifting or sequence errors. However, the homology to the La-protein sequence remains of significant interest. Again, in *Euplotes*, the "UGA" codon encodes a cysteine residue.

#### 20 **EXAMPLE 12: Amino Acid and Nucleic Acid Comparisons**

In this Example, comparisons between various reported sequences and the sequences of the *Euplotes* 123 kDa and 43 kDa telomerase subunit polypeptides were made.

##### **Comparisons with the 123 kDa *E. aediculatus* Telomerase Subunit**

25 The amino acid sequence of the 123 kDa *Euplotes aediculatus* polypeptide was compared with the sequence of the 80 kDa telomerase protein subunit of *Tetrahymena thermophila* (GenBank accession #U25641) to investigate their similarity. The nucleotide sequence as obtained from GenBank (SEQ ID NO:51) encoding this protein is shown in Figure 19. The amino acid sequence of this protein as obtained from  
30 GenBank (SEQ ID NO:52) is shown in Figure 20. The sequence comparison between



the 123 kDa *E. aediculatus* and 80 kDa *T. thermophila* is shown in Figure 13. In this figure, the *E. aediculatus* sequence is the upper sequence (SEQ ID NO:2), while the *T. thermophila* sequence is the lower sequence (SEQ ID NO:52). In this Figure, as well as Figures 14-16, identities are indicated by vertical bars, while single dots between the sequences indicate somewhat similar amino acids, and double dots between the sequences indicate more similar amino acids. The observed identity was determined to be approximately 19%, while the percent similarity was approximately 45%, values similar to what would be observed with any random protein sequence.

The amino acid sequence of the 123 kDa *Euplotes aediculatus* polypeptide was also compared with the sequence of the 95 kDa telomerase protein subunit of *Tetrahymena thermophila* (GenBank accession #U25642), to investigate their similarity. The nucleotide sequence as obtained from GenBank (SEQ ID NO:53) encoding this protein is shown in Figure 21. The amino acid sequence of this protein as obtained from GenBank (SEQ ID NO:54) is shown in Figure 22. This sequence comparison is shown in Figure 14. In this figure, the *E. aediculatus* sequence is the upper sequence (SEQ ID NO:2), while the *T. thermophila* sequence is the lower sequence (SEQ ID NO:54). The observed identity was determined to be approximately 20%, while the percent similarity was approximately 43%, values similar to what would be observed with any random protein sequence.

Significantly, the amino acid sequence of the 123 kDa *E. aediculatus* polypeptide contains the five motifs (SEQ ID NOS:13 and 18) characteristic of reverse transcriptases. The 123 kDa polypeptide was also compared with the polymerase domains of various reverse transcriptases (SEQ ID NOS:14-17, and 19-22). Figure 17 shows the alignment of the 123 kDa polypeptide with the putative yeast homolog (L8543.12 or EST2p)(SEQ ID NOS: 17 and 22). The amino acid sequence of L8543.12 (or EST2p) obtained from GenBank is shown in Figure 23 (SEQ ID NO:55).

Four motifs (A, B, C, and D) were included in this comparison. In this Figure 17, highly conserved residues are indicated by white letters on a black background. Residues of the *E. aediculatus* sequences that are conserved in the other sequence are indicated in bold; the "h" indicates the presence of a hydrophobic amino acid. The

numerals located between amino acid residues of the motifs indicates the length of gaps in the sequences. For example, the "100" shown between motifs A and B reflects a 100 amino acid gap in the sequence between the motifs.

As noted above, Genbank searches identified a yeast protein (Genbank  
5 accession #U20618), and gene L8543.12 (Est2), containing or encoding an amino acid sequence that shows some homology to the *E. aediculatus* 123 kDa telomerase subunit. Based on the observations that both proteins contain reverse transcriptase motifs in their C-terminal regions; both proteins share similarity in regions outside the reverse transcriptase motif; the proteins are similarly basic (pI = 10.1 for *E. aediculatus* and  
10 pI=10.0 for the yeast); and both proteins are large (123 kDa for *E. aediculatus* and 103 kDa for the yeast), these sequences comprise the catalytic core of their respective telomerases. It was contemplated based on this observation of homology in two phylogenetically distinct organisms as *E. aediculatus* and yeast, that human telomerase would contain a protein that has the same characteristics (*i.e.*, reverse transcriptase  
15 motifs, is basic, and large [ $> 100$  kDa]).

#### **Comparisons with the 43 kDa *E. aediculatus* Telomerase Subunit**

The amino acid sequence of the "La-domain" of the 43 kDa *Euplotes*  
*aediculatus* polypeptide was compared with the sequence of the 95 kDa telomerase  
20 protein subunit of *Tetrahymena thermophila* (described above) to investigate their similarity. This sequence comparison is shown in Figure 15. In this figure, the *E. aediculatus* sequence is the upper sequence (SEQ ID NO:9), while the *T. thermophila* sequence is the lower sequence (SEQ ID NO:10). The observed identity was determined to be approximately 23%, while the percent similarity was approximately  
25 46%, values similar to what would be observed with any random protein sequence.

The amino acid sequence of the "La-domain" of the 43 kDa *Euplotes*  
*aediculatus* polypeptide was compared with the sequence of the 80 kDa telomerase  
protein subunit of *Tetrahymena thermophila* (described above) to investigate their  
similarity. This sequence comparison is shown in Figure 16. In this figure, the *E.*  
30 *aediculatus* sequence is the upper sequence (SEQ ID NO:11), while the *T. thermophila*

sequence is the lower sequence (SEQ ID NO:12). The observed identity was determined to be approximately 26%, while the percent similarity was approximately 49%, values similar to what would be observed with any random protein sequence.

The amino acid sequence of a domain of the 43 kDa *E. aediculatus* polypeptide (SEQ ID NO:23) was also compared with La proteins from various other organisms (SEQ ID NOS:24-27). These comparisons are shown in Figure 18. In this Figure, highly conserved residues are indicated by white letters on a black background. Residues of the *E. aediculatus* sequences that are conserved in the other sequence are indicated in bold.

10

**EXAMPLE 13: Identification of Telomerase Protein Subunits in *Oxytricha trifallax***

In this Example, the sequences identified in the previous Examples above were used to identify the telomerase protein subunits of *Oxytricha trifallax*, a ciliate that is very distantly related to *E. aediculatus*. Primers were chosen based on the conserved region of the *E. aediculatus* 123 kDa polypeptide which comprised the reverse transcriptase domain motifs. Suitable primers were synthesized and used in a PCR reaction with total DNA from *Oxytricha*. The *Oxytricha* DNA was prepared according to methods known in the art. The PCR products were then cloned and sequenced using methods known in the art.

20

The oligonucleotide sequences used as the primers were as follows: 5'-(T/C)A(A/G)AC(T/A/C)AA(G/A)GG(T/A/C)AT(T/C)CC(C/T/A)(C/T)A(G/A)GG-3' (SEQ ID NO:56) and 5'-(G/A/T)GT(G/A/T)ATNA(G/A)NA(G/A)(G/A)TA(G/A)TC(G/A)TC-3' (SEQ ID NO:57). Positions that were degenerate are shown in parenthesis, with the alternative bases shown within the parenthesis. "N" represents any of the four nucleotides.

25

In the PCR reaction, a 50 µl reaction contained 0.2 mM dNTPs, 0.3 µg *Oxytricha trifallax* chromosomal DNA, 1 µl *Taq* polymerase (Boehringer-Mannheim), 2 micromolar of each primer, 1x reaction buffer (Boehringer-Mannheim). The reaction was incubated in a thermocycler (Perkin-Elmer) under the following conditions: 5 min

30

at 95EC; 30 cycles consisting of 1 min at 94EC, 1 min at 53EC, and 1 min at 72EC; followed by a 10 min at 72EC. The PCR-product was gel-purified and sequenced by the dideoxy-method (*e.g.*, Sanger (1977) *Proc. Natl. Acad. Sci. USA* 74:5463-5467).

The deduced amino acid sequence of the PCR product was determined and compared with the *E. aediculatus* sequence. Figure 24 shows the alignment of these sequences, with the *O. trifallax* sequence (SEQ ID NO:58) shown in the top row, and the *E. aediculatus* sequence (SEQ ID NO:59) shown in the bottom row. As can be seen from this Figure, there is a great deal of homology between the *O. trifallax* polypeptide sequence identified in this Example with the *E. aediculatus* polypeptide sequence. Thus, it is clear that the sequences identified in the present invention are useful for the identification of homologous telomerase protein subunits in other eukaryotic organisms. Indeed, development of the present invention has identified homologous telomerase sequences in multiple, diverse species, as described above.

#### 15 **EXAMPLE 15 Identification of *Tetrahymena* Telomerase Sequences**

In this Example, a *Tetrahymena* clone was produced that shares homology with the *Euplotes* sequences, and EST2p.

This experiment utilized PCR with degenerate oligonucleotide primers directed against conserved motifs to identify regions of homology between *Tetrahymena*, *Euplotes*, and EST2p sequences. The PCR method used in this Example is a novel method designed to amplify specifically rare DNA sequences from complex mixtures. This method avoids the problem of amplification of DNA products with the same PCR primer at both ends (*i.e.*, single primer products) commonly encountered in PCR cloning methods. These single primer products produce unwanted background and can often obscure the amplification and detection of the desired two-primer product. The method used in this experiment preferentially selects for two-primer products. In particular, one primer is biotinylated and the other is not. After several rounds of PCR amplification, the products are purified using streptavidin magnetic beads and two primer products are specifically eluted using heat denaturation. This method finds use in settings other than the experiments described in this Example. Indeed, this method

finds use in application in which it is desired to specifically amplify rare DNA sequences, including the preliminary steps in cloning methods such as 5' and 3'; RACE, and any method that uses degenerate primers in PCR.

A first PCR run was conducted using *Tetrahymena* template macronuclear DNA isolated using methods known in the art, and the 24-mer forward primer with the sequence 5' biotin-GCCTATTT(TC)TT(TC)TA(TC)(GATC)(GATC)(GATC)AC(GATC)GA-3' (SEQ ID NO:70) designated as "K231," corresponding to the FFYXTE region (SEQ ID NO:71), and the 23-mer reverse primer with the sequence 5'-CCAGATAT(GATC)A(TGA)(GATC)A(AG)(AG)AA(AG)TC(AG)TC- 3' (SEQ ID NO:72), designated as "K220," corresponding to the DDFL(FIL)I region (SEQ ID NO:73). This PCR reaction contained 2.5 µl DNA (50 ng), 4 µl of each primer (20 µM), 3 µl 10x PCR buffer, 3 µl 10x dNTPs, 2 µl Mg, 0.3 µl *Taq*, and 11.2 µl dH<sub>2</sub>O. The mixture was cycled for 8 cycles of 94EC for 45 seconds, 37EC for 45 seconds, and 72 EC for 1 minute.

This PCR reaction was bound to 200 µl streptavidin magnetic beads, washed with 200 µl TE, resuspended in 20 µl dH<sub>2</sub>O and then heat-denatured by boiling at 100EC for 2 minutes. The beads were pulled down and the eluate removed. Then, 2.5 µl of this eluate was subsequently reamplified using the above conditions, with the exception being that 0.3 µl of gamma-<sup>32</sup>P dATP was included, and the PCR was carried out for 33 cycles. This reaction was run a 5% denaturing polyacrylamide gel, and the appropriate region was cut out of the gel. These products were then reamplified for an additional 34 cycles, under the conditions listed above, with the exception being that a 42EC annealing temperature was used.

A second PCR run was conducted using *Tetrahymena* macronuclear DNA template isolated using methods known in the art, and the 23-mer forward primer with the sequence 5'-ACAATG(CA)G(GATC)(TCA)T(GATC)(TCA)T(GATC)CC(GATC)AA(AG)AA-3' (SEQ ID NO:74), designated as "K228," corresponding to the region R(LI)(LI)PKK (SEQ ID NO:75), and a reverse primer with the sequence 5'-ACGAATC(GT)(GATC)GG(TAG)AT(GATC)(GC)(TA)(AG)TC(AG)TA(AG)CA 3' (SEQ ID NO:76), designated "K224," corresponding to the CYDSIPR region (SEQ ID

NO:77). This PCR reaction contained 2.5 µl DNA (50 ng), 4 µl of each primer (20 µM), 3 µl 10x PCR buffer, 3 µl 10x dNTPs, 2 µl Mg, 0.3 µl gamma-<sup>32</sup>P dATP, 0.3 µl *Taq*, and 10.9 µl dH<sub>2</sub>O. This reaction was run on a 5% denaturing polyacrylamide gel, and the appropriate region was cut out of the gel. These products were reamplified for  
5 an additional 34 cycles, under the conditions listed above, with the exception being that a 42EC annealing temperature was used.

Ten µl of the reaction product from run 1 were bound to streptavidin-coated magnetic beads in 200 µl TE. The beads were washed with 200 µl TE, and then then resuspended in 20 µl of dH<sub>2</sub>O, heat denatured, and the eluate was removed. Next, 2.5  
10 µl of this eluate was reamplified for 33 cycles using the conditions indicated above. The reaction product from run 2 was then added to the beads and diluted with 30 µl 0.5x SSC. The mixture was heated from 94EC to 50EC. The eluate was removed and the beads were washed three times in 0.5x SSC at 55EC. The beads were then resuspended in 20 µl dH<sub>2</sub>O, heat denatured, and the eluate was removed, designated as  
15 "round 1 eluate" and saved.

To isolate the *Tetrahymena* band, the round 1 eluate was reamplified with the forward primer K228 (SEQ ID NO:74) and reverse primer K227 (SEQ ID NO:78) with the sequence 5'-CAATTCTC(AG)TA(AG)CA(GATC)(CG)(TA)(CT)TT(AGT)AT(GA)TC-3' (SEQ ID NO:78), corresponding to the DIKSCYD region (SEQ ID  
20 NO:79). The PCR reactions were conducted as described above. The reaction products were run on a 5% polyacrylamide gel; the band corresponding to approximately 295 nucleotides was cut from the gel and sequenced.

The clone designated as 168-3 was sequenced. The DNA sequence (including the primer sequences) was found to be:  
25 GATTACTCCCGAAGAAAGGATCTTTCCGTCCAATCATGACTTTCTTAAGAAA  
GGACAAGCAAAAAAATATTAAGTTAAATCTAAATTAAATTCTAATGGATAG  
CCAAC TTGTGTTTAGGAATTTAAAAGACATGCTGGGATAAAAGATAGGATA  
CTCAGTCTTTGATAATAAACAAATTCAGAAAAATTTGCCTAATTCATAGAG  
AAATGGAAAAATAAAGGAAGACCTCAGCTATATTATGTCACTCTAGACATA  
30 AAGACTTGCTAC (SEQ ID NO:80).

Additional sequence of this gene was obtained by PCR using one unique primer designed to match the sequence from 168-3 ("K297" with the sequence 5'-

GAGTGACATAATATACGTGA-3'; SEQ ID NO:111), and the K231 (FFYXTE)

primer. The sequence of the fragment obtained from this reaction, together with 168-3

5 is as follows (without the primer sequences):

AAACACAAGGAAGGAAGTCAAATATTCTATTACCGTAAACCAATATGGAA  
 ATTAGTGAGTAAATTAAGTATTGTCAAAGTAAGAATTTAGTTTTCTGAAAAG  
 AATAAATAAATGAAAAATAATTTTTATCAAAAAATTTAGCTTGAAGAGGAG  
 AATTTGGAAAAAGTTGAAGAAAAATTGATACCAGAAGATTCATTTTAGAAA  
 10 TACCCTCAAGGAAAGCTAAGGATTATACCTAAAAAAGGATCTTTCCGTCCA  
 ATCATGACTTTCTTAAGAAAGGACAAGCAAAAAATATTAAGTTAAATCTA  
 AATTAAATTCTAATGGATAGCCAACTTGTGTTTAGGAATTTAAAAGACATG  
 CTGGGATAAAAGATAGGATACTCAGTCTTTGATAATAAACAAATTCAGAA  
 AAATTTGCCTAATTCATAGAGAAATGGAAAAATAAAGGAAGACCTCAGCTA  
 15 TATTATGTCACTCTA (SEQ ID NO:81).

The amino acid sequence corresponding to this DNA fragment was found to be:

KHKEGSQIFYRKPIWKLVSCLTIVKVRIOFSEKNKQMKNNFYQKIQLEENLE  
 KVEEKLIPEDSFQKYPQGKLRIIPKKGSRPIMTFLRKDKQKNIKLNLNQILMDS  
 QLVFRNLKDMLGQKIGYSVFDNKQISEKFAQFIEKWKNKGRPQLYYVTL (SEQ

20 ID NO:82).

This amino acid sequence was then aligned with other telomerase genes (EST2p, and *Euplotes*). The alignment is shown in Figure 31. A consensus sequence is also shown in this Figure.

#### 25 **EXAMPLE 16: Identification of *Schizosaccharomyces pombe* Telomerase Sequences**

In this Example, the *tez1* sequence of *S. pombe* was identified as a homolog of the *E. aedicularis* p123, and *S. cerevisiae* Est2p.

Figure 33 provides an overall summary of these experiments. In this Figure, the  
 30 top portion (Panel A) shows the relationship of two overlapping genomic clones, and

the 5825 bp portion that was sequenced. The region designated at "tez1<sup>+</sup>" is the protein coding region, with the flanking sequences indicated as well, the box underneath the 5825 bp region is an approximately 2 kb *Hind*III fragment that was used to make the tez1 disruption construct, as described below.

5        The bottom half of Figure 33 (Panel B) is a "close-up" schematic of this same region of DNA. The sequence designated as "original PCR" is the original degenerate PCR fragment that was generated with a degenerate oligonucleotide primer pair designed based on *Euplotes* sequence motif 4 (B') and motif 5 (C), as described.

#### PCR With Degenerate Primers

10        PCR using degenerate primers was used to find the homolog of the *E. aediculatus* p123 in *S. pombe*. Figure 34 shows the sequences of the degenerate primers (designated as "poly 4" and "poly 1") used in this reaction. The PCR runs were conducted using the same buffer as described in previous Examples (*See e.g.*, Example 10, above), with a 5 minute ramp time at 94EC, followed by 30 cycles of 94EC for 30  
15        seconds, 50EC for 45 seconds, and 72EC for 30 seconds, and 7 minutes at 72EC, followed by storage at 4EC. PCR runs were conducted using varied conditions, (*i.e.*, various concentrations of *S. pombe* DNA and MgCl<sub>2</sub> concentrations). The PCR products were run on agarose gels and stained with ethidium bromide as described above. Several PCR runs resulted in the production of three bands (designated as "T,"  
20        "M," and "B"). These bands were re-amplified and run on gels using the same conditions as described above. Four bands were observed following this re-amplification ("T," "M1," "M2," and "B"), as shown in Figure 35. These four bands were then re-amplified using the same conditions as described above. The third band from the top of the lane in Figure 35 was identified as containing the correct sequence  
25        for a telomerase protein. The PCR product designated as M2 was found to show a reasonable match with other telomerase proteins, as indicated in Figure 36. In addition to the alignment shown, this Figure also shows the actual sequence of *tez1*. In this Figure, the asterisks indicate residues shared with all four sequences (*Oxytricha* "Ot"; *E. aediculatus* "Ea\_p123"; *S. cerevisiae* "Sc\_p103"; and M2), while the circles (*i.e.*,  
30        dots) indicate similar amino acid residues.



### 3' RT PCR

To obtain additional sequence information, 3' and 5' RT PCR were conducted on the telomerase candidate identified in Figure 36. Figure 37 provides a schematic of the 3' RT PCR strategy used. First, cDNA was prepared from mRNA using the  
5 oligonucleotide primer "Q<sub>T</sub>" (5'-CCA GTG AGC AGA GTG ACG AGG ACT CGA GCT CAA GCT TTT TTT TTT TTT TT-3'; SEQ ID NO:102), then using this cDNA as a template for PCR with "Q<sub>0</sub>" (5'-CCA GTG AGC AGA GTG ACG-3'; SEQ ID NO:103), and a primer designed based on the original degenerated PCR reaction (*i.e.*, "M2-T" with the sequence 5'-G TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT  
10 G-3' (SEQ ID NO:109). The second PCR reaction (*i.e.*, nested PCR) with "Q<sub>1</sub>" (5'-GAG GAC TCG AGC TCA AGC-3'; SEQ ID NO:104), and another PCR primer designed with sequence derived from the original degenerate PCR reaction or "M2-T2" (5'-AC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG-3'; SEQ ID NO:110). The buffers used in this PCR were the same as described above, with amplification  
15 conducted beginning with a ramp up of 94E for 5 min, followed by 30 cycles of 94E for 30 sec, 55EC for 30 sec, and 72EC for 3 min), followed by 7 minutes at 72EC. The reaction products were stored at 4EC until use.

### Screening of Genomic and cDNA Libraries

After obtaining this additional sequence information, several genomic and  
20 cDNA libraries were screened to identify any libraries that contain this telomerase candidate gene. The approach used, as well as the libraries and results are shown in Figure 38. In this Figure, Panel A lists the libraries tested in this experiment; Panel B shows the regions used; Panels C and D show the dot blot hybridization results obtained with these libraries. Positive libraries were then screened by colony  
25 hybridization to obtain genomic and cDNA version of *tez1* gene. In this experiment, approximately  $3 \times 10^4$  colonies from the *HindIII* genomic library were screened and six positive clones were identified (approximately 0.01%). DNA was then prepared from two independent clones (A5 and B2). Figure 39 shows the results obtained with the *HindIII*-digested A5 and B2 positive genomic clones.

In addition, cDNA REP libraries were used. Approximately  $3 \times 10^5$  colonies were screened, and 5 positive clones were identified (0.002%). DNA was prepared from three independent clones (2-3, 4-1, and 5-20). In later experiments, it was determined that 2-3 and 5-20 contained identical inserts.

## 5 5' RT PCR

As the cDNA version of gene produced to this point was not complete, 5' RT-PCR was conducted to obtain a full length clone. The strategy is schematically shown in Figure 40. In this experiment, cDNA was prepared using DNA oligonucleotide primer "M2-B" (5'-CAC TGA TCC TTT CTT TTT CGT AAA CGA TAG GT-3'; SEQ ID NO:105) and "M2-B2" (5'-C ATC AAT CAA ATC TTC CAT ATA GAA ATG ACA-3'; SEQ ID NO:106), designed from known regions of *tez1* identified previously. An oligonucleotide linker PCR Adapt SfiI with a phosphorylated 5' end ("P") (P-GGG CCG TGT TGG CCT AGT TCT CTG CTC-3'; SEQ ID NO:107) was then ligated at the 3' end of this cDNA, and this construct was used as the template for nested PCR. In the first round of PCR, PCR Adapt SFI and M2-B were used as the primers; while PCR Adapt SfiII (5-GAG GAG GAG AAG AGC AGA GAA CTA GGC CAA CAC GCC CC-3'; SEQ ID NO:108), and M2-B2 (SEQ ID NO:106) were used as primers in the second round. Nested PCR was used to increase specificity of reaction.

## 20 Sequence Alignments

Once the sequence of *tez1* was identified, it was compared with sequences previously described. Figure 41 shows the alignment of RT domains from telomerase catalytic subunits of *S. pombe* ("S.p. Tez1p"), *S. cerevisiae* ("S.c. Est2p"), and *E. aediculatus* p123 ("E.a. p123"). In this Figure, "h" indicates hydrophobic residues, while "p" indicates small polar residues, and "c" indicates charged residues. The amino acid residues indicated above the alignment show a consensus RT motif described by Xiong (1990) *EMBO J.* 9: 3353-3362. The asterisks indicate the residues that are conserved for all three proteins. "Motif O" is identified herein and in Figure 41 as a motif specific to this telomerase subunit and not found in reverse transcriptases in

general. It is therefore valuable in identifying other amino acid sequences as telomerase catalytic subunits.

Figure 42 shows the alignment of entire sequences from *Euplotes* ("Ea\_p123"), *S. cerevisiae* ("Sc\_Est2p"), and *S. pombe* ("Sp\_Tez1p"). In Panel A, the shaded areas indicate residues shared between two sequences. In Panel B, the shaded areas indicate residues shared between all three sequences.

#### Genetic Disruption of *tez1*

In this Example, the effects of disruption of *tez1* were investigated. As telomerase is involved in telomere maintenance, it was hypothesized that if *tez1* were indeed a telomerase component, disruption of *tez1* would cause gradual telomere shortening.

In these experiments, homologous recombination was used to disrupt the *tez1* gene in *S. pombe* specifically. This approach is schematically illustrated in Figure 43. As indicated in Figure 43, wild type *tez1* was replaced with a fragment containing the *ura4* or *LEU2* marker.

The disruption of *tez1* gene was confirmed by PCR (Figure 44), and Southern blot was performed to check for telomere length. Figure 45 shows the Southern blot results for this experiment. Because an *ApaI* restriction enzyme site is present immediately adjacent to telomeric sequence in *S. pombe*, *ApaI* digestion of *S. pombe* genomic DNA preparations permits analysis of telomere length. Thus, DNA from *S. pombe* was digested with *ApaI* and the digestion products were run on an agarose gel and probed with a telomeric sequence-specific probe to determine whether the telomeres of disrupted *S. pombe* cells were shortened. The results are shown in Figure 45. From these results, it was clear that disruption of the *tez1* gene caused a shortening of the telomeres.

#### **EXAMPLE 17: Cloning and Characterization of Human Telomerase Reverse Transcriptase Protein and cDNA**

In this Example, the nucleic and amino acid sequence information for human telomerase reverse transcriptase was determined. Partial homologous human sequences

were first identified in a BLAST search of the dbEST (expressed sequence tag) Genbank database, designated Genbank AA28196 (SEQ ID NO:121), which was conducted using the *Euplotes* 123 kDa peptide and nucleic acid sequences, as well as *Schizosaccharomyces* protein and corresponding cDNA (tez1) sequences. EST  
 5 GenBank accession #AA281296, also referred to as "hTCP1.1," is a partial cDNA clone.

The AA281296 EST (SEQ ID NO:121) is 389 nucleotides long and its residue positions in hTRT cDNA clone (SEQ ID NO:117) are from residues 1679 to 2067:

```

10                                     1679
                                           G GTTGGCTGTG TTCCGGCCGC
AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCCTG CACTGGCTGA 1700
TGAGTGTGTA CGTCGTCGAG CTGCTCAGGT CTTTCTTTTA TGTCACGGAG 1750
ACCACGTTTC AAAAGAACAG GCTCTTTTTC TACCGGAAGA GTGTCTGGAG 1800
CAAGTTGCAA AGCATTGGAA TCAGACAGCA CTTGAAGAGG GTGCAGCTGC 1850
15 GGGAGCTGTC GGAAGCAGAG GTCAGGCAGC ATCGGGAAGC CAGGCCCCGCC 1900
CTGCTGACGT CCAGACTCCG CTTTCATCCCC AAGCCTGACG GGCTGCGGCC 1950
GATTGTGAAC ATGGACTACG TCGTGGGAGC CAGAACGTTT CGCAGAGAAA 2000
AGAGGGCCGA GCGTCTCACC TCGAGGGTGA AGGCACTGTT CAGCGTGCTC 2050
AACTACGAGC GGGCGCGGCG CCCC GGCCCTC CTGGGCGCCT CTGTGCTGGG 2100
20 CCTGGACGAT ATCCACAG
2150                               |2067 (SEQ ID NO:121)
  
```

A clone containing the AA28196 EST sequence, designated clone #712562 (SEQ ID NO:122), was obtained from the I.M.A.G.E. Consortium (Human Genome  
 25 Center, DOE, Lawrence Livermore National Laboratory, Livermore, CA). This clone was obtained from a cDNA library of germinal B cells derived by flow sorting of tonsil cells. Complete sequencing of this hTRT cDNA clone #712562 (SEQ ID NO:122, Figure 59), and analysis of the deduced translation product (SEQ ID NO:123, Figure 59) showed that it encoded all eight telomerase RT (TRT) motifs, as shown in Figure 1.  
 30 In contrast to the polypeptide encoded by the hTRT open reading frame of the cDNA in pGRN121 (discussed below), clone #712562 did not encode a contiguous portion of a TRT, because 182 base pairs are missing in clone 712562 that are present in the hTRT

encoded in pGRN121. The coding sequence in clone #712562 encodes a 259 residue protein with a calculated molecular weight of approximately 30 kD (hereinafter, "712562 hTRT"). The 712562 hTRT polypeptide contains motifs T, 1,2, and A, but not motifs B', C, D and E, because RT motifs B', C, D, and E, are contained in a different open reading frame than the more N-terminal RT motifs. In addition, the distance between RT motifs A and B was substantially shorter than that of the three previously known (non-human) TRTs.

Amino acid sequences from clone #712562 (SEQ ID NO:123) were aligned with the sequences determined as described in previous Examples. Figure 25 shows the sequence alignment of the *Euplotes* ("p123"), *Schizosaccharomyces* ("tez1"), Est2p (*i.e.*, the *S. cerevisiae* protein encoded by the *Est2* nucleic acid sequence, and also referred to herein as "L8543.12"), and the human homolog identified in this comparison search. The amino acid sequence of this aligned portion is provided in SEQ ID NO:61 (the cDNA sequence is provided in SEQ ID NO:62), while the portion of *tez1* shown in Figure 25 is provided in SEQ ID NO:63. The portion of Est2 shown in this Figure is also provided in SEQ ID NO:64, while the portion of p123 shown is also provided in SEQ ID NO:65. Figure 29 shows the amino acid sequence of *tez1* (SEQ ID NO:68), while Figure 30 shows the DNA sequence of *tez1* (SEQ ID NO:69). In Figure 30, the introns and other non-coding regions, are shown in lower case, while the exons (*i.e.*, coding regions) are shown in upper case.

As shown in Figure 25, there are regions that are highly conserved among these proteins. For example, as shown in this Figure, there are regions of identity in "Motif 0," "Motif 1," "Motif 2," and "Motif 3." The identical amino acids are indicated with an asterisk (\*), while the similar amino acid residues are indicated by a dot ( . ). This indicates that there are regions within the telomerase motifs that are conserved among a wide variety of eukaryotes, ranging from yeast to ciliates to humans. It is contemplated that TRT genes of additional organisms will likewise contain such conserved regions of sequence. Figure 27 shows a partial amino acid sequence (SEQ ID NO:67, see also Figure 25, SEQ ID NO:61) of clone #712562 (SEQ ID NO:123) which encodes human

telomerase motifs, while Figure 28 shows the corresponding DNA sequence (SEQ ID NO:62).

Sanger dideoxy sequencing and other methods were used as known in the art to obtain complete sequence information of clone 712562. Some of the primers used in the sequencing are shown in Table 3. These primers were designed to hybridize to the clone based on sequence complementarity to either plasmid backbone sequence or the sequence of the human cDNA insert in the clone.

**Table 3. Primers**

Primer	Sequence	SEQ ID NO:
TCP1.1	GTGAAGGCACTGTTCA GCG	SEQ ID NO:87
TCP1.2	GTGGATGATTTCTTGT TGG	SEQ ID NO:88
TCP1.3	ATGCTCCTGCGTTTG GTGG	SEQ ID NO:89
TCP1.4	CTGGACACTCAGCCCT TGG	SEQ ID NO:90
TCP1.5	GGCAGGTGTGCTGGAC ACT	SEQ ID NO:91
TCP1.6	TTTGATGATGCTGGCG ATG	SEQ ID NO:92
TCP1.7	GGGGCTCGTCTTCTAC AGG	SEQ ID NO:93
TCP1.8	CAGCAGGAGGATCTTG TAG	SEQ ID NO:94
TCP1.9	TGACCCCAGGAGTGGC ACG	SEQ ID NO:95
TCP1.10	TCAAGCTGACTCGACAC CG	SEQ ID NO:96
TCP1.11	CGGCGTGACAGGGCTGC	SEQ ID NO:97
TCP1.12	GCTGAAGGCTGAGTGTCC	SEQ ID NO:98
TCP1.13	TAGTCCATGTTCA CAATCG	SEQ ID NO:99

From these experiments, it was determined that the EcoRI-NotI insert of clone 712562 contains only a partial open reading frame for the human telomerase protein, although it may encode an active fragment of that protein. The open reading frame in the AA281296 clone encodes an approximately 63 kD protein. The sequence of the longest open reading frame identified is shown in Figure 47 (SEQ ID NO:100). The

ORF begins at the ATG codon with the "met" indicated in the Figure. The poly A tail at the 3' end of the sequence is also shown.

Figure 48 shows a tentative alignment, based on a preliminary sequence analysis, of the telomerase reverse transcriptase protein coding sequence from clone 5 712562 (human Telomerase Core Protein 1, "Hs TCP1"), *E. aediculatus* p123 ("Ep p123"), *S. pombe* tez1 ("Sp Tez1"), *S. cerevisiae* EST2 (Sc Est2"), and consensus sequence. In this Figure various motifs are indicated.

To obtain a full-length clone, probing of a cDNA library and 5'-RACE were used to obtain clones encoding portions of the previously uncloned regions. In these 10 experiments, RACE (Rapid Amplification of cDNA Ends; *See e.g., M.A. Frohman, "RACE: Rapid Amplification of cDNA Ends," in Innis et al. (eds), PCR Protocols: A Guide to Methods and Applications* [1990], pp. 28-38; and Frohman *et al.*, *Proc. Natl. Acad. Sci.*, 85:8998-9002 [1988]) was used to generate material for sequence analysis. Four such clones were generated and used to provide additional 5' sequence 15 information (pFWRP5, 6, 19, and 20).

In addition, human cDNA libraries (inserted into lambda) were probed with the EcoRI-NotI fragment of clone 712562 (containing AA281296). One lambda clone, designated "lambda 25-1.1," (ATCC accession # 209024) was identified as containing complementary sequences. Figure 54 shows a restriction map of this lambda clone. 20 The human cDNA insert from this clone was subcloned as an *EcoRI* restriction fragment into the *EcoRI* site of commercially available phagemid pBluescriptII SK+ (Stratagene), to create the plasmid "pGRN121," which was deposited with the ATCC (ATCC accession #209016). Preliminary results indicated that plasmid pGRN121 contains the entire open reading frame (ORF) sequence encoding the human telomerase 25 protein.

The cDNA insert of plasmid pGRN121 was sequenced using techniques known in the art. Figure 49 provides a restriction site and function map of plasmid pGRN121 identified based on this preliminary work. The results of this preliminary sequence analysis are shown in Figure 50.

From this analysis, and as shown in Figure 49, a putative start site for the coding region was identified at approximately 50 nucleotides from the *EcoRI* site (located at position 707), and the location of the telomerase-specific motifs, "FFYVTE" (SEQ ID NO:112), "PKP," "AYD," "QG", and "DD," were identified, in addition to a putative stop site at nucleotide #3571 (See, Figure 51). Figure 51 shows the DNA and corresponding amino acid sequences for the open reading frames in the sequence ("a" (SEQ ID NO:114), "b" (SEQ ID NO:115), and "c" (SEQ ID NO:116)). However, due to the preliminary nature of the early sequencing work, the reading frames for the various motifs were found not to be in alignment.

Additional analysis conducted on the pGRN121 indicated that the plasmid contained significant portions from the 5'-end of the coding sequence not present on the 712562 clone. Furthermore, pGRN121 was found to contain a variant coding sequence that includes an insert of approximately 182 nucleotides. This insert was found, as noted above, to be absent from clone 712562. As with the *E. aedicularis* sequences, such variants can be tested in functional assays, such as telomerase assays, to detect the presence of functional telomerase or a partial TRT activity in a sample.

A preliminary sequence analysis showed cDNA sequence and an open reading frame (SEQ ID NO:119 and 120, respectively, as shown in Figure 58). Further sequence analysis resolved the cDNA sequence (nucleotide sequence) of pGRN121, as shown in Figure 53 (SEQ ID NOS:117). A refined restriction and function map of pGRN121 based on this analysis, is provided in Figure 52. Analysis of this cDNA shows a contiguous open reading frame encoding a protein of molecular weight of approximately 127,000 daltons, and 1132 amino acids (SEQ ID NO:118):

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDA  
 RPPPAAPSFQVSKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTV  
 TDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGAATQARPPPHA  
 SGPRRRLGCERAWNHISVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQG  
 SWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDT  
 PCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQR  
 YWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRLR  
 VQLLRQHSSPWQVYGFVRACLRLVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQELTWK



MSVRDCAWLRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFF  
 YRKS VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPA LLTSRLRFIPKPDGLRPVNM DYVV  
 GARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPP  
 ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTD  
 5 LQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIQ  
 GSILSTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVV  
 NLRKTVVNFVVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTfNR  
 GFKAGRNMRRKLFGVLR LKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQQV  
 WKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTY  
 10 VP LLGSLRTAQTQLSRKLP GTTLTALEAAANPALPSDFKTILD SEQ ID NO:118

A variant hTRT polypeptide with therapeutic and other activities may be expressed from a nucleic acid similar to the pGRN121 cDNA but lacking the 182 base pairs missing in clone 712562 (SEQ ID NO:122). This nucleic acid (hereinafter, "pro90 hTRT"), which may be synthesized using routine synthetic or recombinant methods as described herein, encodes a protein of 807 residues (calculated molecular weight of approximately 90 kD) that shares the same amino terminal sequence as the hTRT protein encoded by SEQ. ID. NO:118, but diverges at the carboxy-terminal region (the first 763 residues are common, the last 44 residues of pro90 hTRT are different than "full-length" hTRT). The pro90 hTRT polypeptide contains motifs T, I, 2, and A, but not motifs B, C, D, E, and is thus expected to have some, but not all telomerase activities.

The invention provides still other recombinant, isolated or purified forms of naturally occurring hTRT species or non-naturally occurring variants. One example of a naturally occurring hTRT species not previously discussed results from ribosome frameshifting of mRNA encoded by the clone 712562 (SEQ ID NO:122) or hTRT cDNA (SEQ. ID. NO:117) sequence may result in the synthesis of hTRT polypeptides containing all the TRT motifs (see, e.g., Tsuchihashi (1990) *Proc. Nat'l. Acad. Sci. USA* 87:2516; Craigengen (1987) *Cell* 50:1; Weiss (1990) *Cell* 62:117). Ribosome frameshifting occurs when specific mRNA sequences and secondary structures cause the ribosome to "stall" and jump one nucleotide forwards or back in the sequence.

Thus, a ribosome frameshift event on an mRNA corresponding to the hTRT sequence of clone 712562 would cause the synthesis of an approximately 523 residue polypeptide. A ribosome frameshift event on the pro90 sequence would result in a protein with approximately 1071 residues. It will be appreciated that hypothetical  
5 proteins resulting from ribosome frameshifting can also be expressed by routine synthetic or recombinant techniques.

#### **Example 18. Cloning and Sequencing Species of Telomerase**

The invention provides a genus of telomerases including telomerase species of human and non-human origin. The invention provides examples of a representative  
10 number of telomerase species of the genus and a recitation of structural features common to the members of the genus to be used in the detection and identification of telomerase isoforms and homologs and telomerases of other species and genera of eukaryotic organisms. Members of the genus of telomerase species of the instant  
15 invention include telomerase isolated from *Euplotes aediculatus* p123 gene (SEQ ID NO:1), *Oxytricha* (encoding SEQ ID NO:58), *Saccharomyces cerevisiae* (SEQ ID NO:66), *Tetrahymena*, and *Schizosaccharomyces pombe*, *trl1* (SEQ ID NO:69).

The present invention provides reagents and methods for identifying and cloning novel TRTs using: nucleic acid probes and primers generated or derived from  
20 the TRT polynucleotides for cloning TRT genes and cDNAs; and, antibodies that specifically recognize TRTs, including the motifs or other TRT epitopes for expression cloning of TRT genes or identification and purification of the genus of TRT polypeptides.

The hTRT nucleic acid sequence (from cDNA of SEQ ID NO:117) and protein  
25 sequence information (SEQ ID NO:118) provide PCR primers and oligonucleotides for the identification of telomerase gene(s) and cDNA. PCR primer pairs that can amplify sequences conserved amongst members of the TRT genus are preferred reagents of the invention to amplify new TRT isoforms and TRT species from other organisms directly.

Alternatively, oligonucleotides are useful to detect telomerase-encoding nucleic acids using a variety of hybridization techniques and conditions. These oligonucleotides can be generated using any known technique, including PCR, enzymatic restriction digestion of isolated DNA, or organic synthesis. These nucleic acids are labeled for  
5 detection and hybridized to DNA by any known technique, as described above.

Total RNA is extracted and enriched for mRNA using the QuickPrep Micro mRNA Purification Kit (Pharmacia, Piscataway, NJ) according to the manufacturer's instructions. The mRNA is then used to make cDNA templates by reverse transcription using, for example, the avian myeloblastosis virus (AMV) reverse transcriptase  
10 (Pharmacia) as described by Sambrook. PCR is performed on the cDNA using, for example, a Techne PHC-3 thermal cycler (Techne, Princeton, NJ) using any set of primers whose sequence is based on a known hTERT sequence. PCR can also be used to amplify telomerase sequences from genomic DNA. Alternative variations of traditional PCR can be used, such as RACE, as described above. PCR amplification can use a  
15 variety of annealing conditions. For example, hTERT is amplified using the following cycling protocol: denaturing at 94°C, 45 seconds; annealing at 60°C, 45 seconds; and extension at 72°C, 90 seconds. This is repeated for a total of about 30 to 40 cycles, yielding a DNA product, which is purified. The PCR product can be sequenced by any known technique, such as the dideoxy-chain termination method using a Dye  
20 Terminator Cycle Sequencing Kit™ Ready Reaction Kit (Applied Biosystems, Foster City, CA) and a Model 373A DNA Sequencer (Applied Biosystems). The PCR product, once identified as a human telomerase sequence, is further labeled and used as a hybridization probe, as described above.

The invention provides for probes of TRT that are particularly useful for  
25 screening, including full length TRT cDNA (*i.e.*, SEQ ID NOS:1, 3, 53, 55, 117) and various fragments of TRT cDNA. One such probe includes a portion of TRT encompassing approximately the first third of the cDNA (SEQ ID NO:117) (Figure 53). This region is more GC rich than the rest of TRT and can be especially useful in detecting non-human telomerase sequences. Therefore one can screen with probes to  
30 this region to minimize unwanted clones. Useful examples of this region include: a

1203 base pair Eco47 III fragment of pGRN121 (position 729 to 1932 of SEQ ID NO:117), and a 1530 base pair Pml1/Sph1 fragment of pGRN121 (position 748 to 2278 of SEQ ID NO:117).

Another embodiment provides for a probe including a portion of TRT encompassing approximately the middle third of a TRT cDNA (*i.e.*, SEQ ID NO:117). This region encodes the RT motifs and is believed to be a highly conserved region. A useful example of the telomerase RT region includes a 1143 bp Sph1/Xmn1 fragment of pGRN121 (position 2278 to 3421 of SEQ ID NO:117).

An additional embodiment provides for a probe that is a portion of TRT encompassing approximately the last third of the TRT cDNA (*i.e.*, SEQ ID NO:117). This region encodes the region of hTRT that is least conserved among TRTs. A useful example of this region includes a 760 bp Xmn1/Msc1 fragment of pGRN121 (position 3421 to 4594 of SEQ ID NO:117).

The experiment can be performed with a mix of the probes to ensure the detection of at least one clone. Once a clone is identified it can be screened with each probe independently to identify the region it encompasses. Then the probes can be used independently to find other related regions. When a clone is identified, a screen of a mouse (and other mammalian) genomic library can be performed using the mTRT clone as a probe. The initial hybridization using TRT probes should be performed at reduced stringency. As isoforms of TRT genes are expected to be about 60-95% identical to the TRT probe sequence, appropriate hybridization conditions are calculated; see for example, Sambrook.

Computer databases and programs can be used to analyze the resultant DNA sequence for its sequence identity, or homology, to known telomerase sequences, as described above. For example, PC/GeneTM software (IntelliGenetics Inc., Mountain View, CA) aligns sequences and displays open reading frames. BLAST N and BLAST D search algorithms can be employed to search the GenBank database (NIH, Bethesda, MD) for any matches between the derived telomerase sequence and known sequences.

### Cloning of Mouse Telomerase-Encoding Sequences

The hTERT and other TERT polynucleotides (e.g., *Euplotes* 123 and 43 kDa encoding sequences, pGRN121) can be used to clone homologous TERTs from other species. In this example, the cloning of mouse TERT using hTERT probes is described.

5 To obtain a clone of telomerase from another organism, a hybridization experiment is typically performed. A probe from a TERT, which could be a PCR fragment(s) of a TERT cDNA or a region of a TERT gene, or a restriction fragment(s) of a plasmid, such as pGRN121, that includes all or part of a TERT coding sequence, is hybridized to DNA from the target organism. Alternatively, as described above,  
10 antibody probes can be used.

A mouse TERT cDNA clone was obtained by plaque screening of a mouse lambda gt10 cDNA library (made using RNA from the D3 line of pluripotent embryonic stem cells) using a 1203 bp Eco47 III fragment of pGRN121 (position 729 to 1932 of pGRN121) and a 1143 bp SphI/XmnI fragment of pGRN121 (position 2278 to 3421 of  
15 pGRN121) as probes. The mouse TERT (mTERT) clone sequence was subcloned into the EcoRI site of pBluescript II KS (Stratagene, San Diego, CA). The subclone was sequenced and approximately 2 kilobases of 5' sequence obtained (nucleotides 1-2009 of SEQ ID NO:124, as shown in Figure 60).

PCR amplification of mouse cDNA generated from oligo-dT primed mouse  
20 testis RNA was used to clone additional mTERT gene sequence. The primers used were mTERT.9 (5'-CTTTTACATCACAGAGAGCAC) (SEQ ID NO:125) and hTERT.28 (5'-CTCGGACCAGGGTCCTGAGGAA) (SEQ ID NO:126). Probe mTERT.9 was designed to position 1682-1702 of mTERT (Figure 60). Probe hTERT.28 was designed to position 2702-2723 of hTERT. The amplification of the mouse TERT gene using a primer  
25 designed from human TERT gene sequence is illustrative of the utility of the TERT sequences or the invention in obtaining clones from other organisms, especially mammals, such as mice, and other non-human animals (such as primates). The amplified DNA was cloned and sequenced (nucleotides 1682-2695 of SEQ ID NO:124, as shown in Figure 60).

Additional mTRT sequence was obtained from a BAC clone identified by hybridization screening of a pooled BAC library using a 760 bp XmnI/MscI fragment of pGRN121 (position 3421 to 4181 of pGRN121). A 1.3 Kb PstI fragment from a positive BAC clone (BAC 495-M5) was identified as containing mTRT coding  
5 sequence by a Southern hybridization experiment using the 760 bp XmnI/MscI fragment as a probe. The PstI fragment was subcloned into the PstI site of pBluescript II KS (Stratagene) and sequenced (nucleotides 2890-3025 of SEQ ID NO:124, as shown in Figure 60). The additional portion of clone 495-2A2 contains a sequence non-homologous to hTRT and is believed to be an intron or vector sequence.

10 In Figure 60, "X"s represent uncloned regions of the mTRT gene and "Xs" represent cloned but unsequenced regions (with lengths determined by analogy to hTRT). The mTRT gene sequence can be extended to encode the carboxyl terminus of mTRT protein plus and a 3' untranslated region by standard methods known in the art.

#### 15 *Applications of Mouse Telomerase-Encoding Sequences*

Mouse cDNA and genomic clones of telomerase are provided by the invention and can be used to construct homozygous deletions of mTRT; characterize mTRT biochemistry and biology; construct knockouts of both mTRT and the mouse equivalent of hTR (mTR); and, express hTRT and hTR in mouse transgenic knockouts  
20 of mTRT or mTRT/mTR. The mouse DNA could be genomic DNA, a genomic DNA library, RNA, cDNA, a cDNA library, or others. In one embodiment, a mouse cDNA library is screened to obtain a fragment of mTRT cDNA. This sequence can in turn be used to find a genomic clone or further cDNA clones. This approach may be preferred in the event the hTRT probe hybridizes to mouse cDNA than mouse genomic DNA due  
25 to introns in the genomic DNA library. The source of the cDNA library is important; it should preferably be from a tissue known to possess telomerase activity. A mouse embryonic stem cell cDNA library is a particularly good choice, as expression of telomerase in stem cells is relatively high compared to normal diploid cells.

30 The mouse genomic clone provides constructs useful to target and knockout the mTRT gene, in accordance with the discussion above concerning knockout procedures.

To clone an entire telomerase gene, such as mTRT, large multiple genomic lambda clones can be used to span the entire genomic sequence. The mouse ES library used to isolate the mouse clone was the Mouse Embryonic Stem Cell 5'-STRETCH cDNA library, cat # ML1049a, from CLONTECH, average insert size 1.6 Kb (0.8 - 4.5 Kb range), vector = lgt10, oligo dT and random hexamer primed with EcoR I linkers, RNA source = D3 cell line (pluripotent ES cells) (Doetschman, T.C., et al. (1985) J. Embryol. Exp. Morphol. 87:27-45).

**Example 18. Identification of the Human Homologue of 43 kDa Telomerase**

10       The *Euplotes aediculatus* polynucleotide sequence (SEQ ID NO:3) encoding the 43 kDa polypeptide (SEQ ID NO:4-6 and SEQ ID NO:9) can be used to clone homologous TRTs from other species. Furthermore, antibodies that specifically recognize TRTs, including the 43 kDa TRT, can be used to identify additional isoforms and species from other organisms. The scientific and patent literature describes use of  
15       antibodies to identify closely related, cross-reactive species using a variety of techniques, for example, expression cloning of TRT genes or identification and purification of 43 kDa TRT polypeptides can be used to isolate the human homologue of the *Euplotes* p43 (43kDa) telomerase subunit gene.

      In this illustrative example, the cloning of the gene encoding the human  
20       homologue of the *E. aediculatus* 43 kDa (p43) TRT using *E. aediculatus* oligonucleotide probes and antibodies reactive with *E. aediculatus* 43 kDa TRT is described.

***Production of 43 kDa-Specific Antibodies***

25       For generation of an antibody reactive with 43 kDa polypeptides, the following peptide was designed for use as an immunogen: CGGQKQLEFYFSDANLYNDSFL (SEQ ID NO:127). This peptide was conjugated to KLH (keyhole limpet hemocyanin) and BSA (bovine serum albumin). The peptide immunogen was used to generate murine and rabbit polyclonal antisera. After only two bleeds, the antisera with the  
30       highest titer was  $4.1 \times 10^4$ . The animals were boosted, using the same protocol. Peak

bleed titers were at  $8 \times 10^5$  or better. Antibodies are isolated from the antisera using using conventional techniques, such as immunogen peptide affinity columns. Monoclonal antibodies reactive to 43 kDa polypeptides are generated using standard techniques, including techniques which select antibodies from libraries of recombinant antibodies displayed in phage or similar on cells, as discussed above.

#### **Example 19: Design and Production of Yeast TRT-Specific Peptides**

The *S. cerevisiae* TRT polynucleotide sequence (SEQ ID NO:66) encoding the yeast TRT polypeptide (SEQ ID NO:64) can be also be used to clone homologous TRTs from other species. Antibodies that specifically recognize yeast TRT can be used to identify additional TRT isoforms and species from other organisms. In this illustrative example, antibodies specific for the yeast TRT polypeptides are generated.

For generation of an antibody reactive with *S. cerevisiae* TRT polynucleotide, the following peptide was designed for use as an immunogen:

NFNHSKMRIIPKKSNEFR II (designated "yIPKK") (SEQ ID NO:128) and CLPELYFMKFDVKSCYDSIPRMECMRILK (designated "yCYDS") (SEQ ID NO:129). These peptides were conjugated to KLH (keyhole limpet hemocyanin) and BSA (bovine serum albumin). The peptide immunogens were used to generate murine and rabbit polyclonal antisera.. The animals were immunized and boosted using the same protocol described for generation of *Euplotes* anti-p43 (43kDa) antibodies. Peak bleed titers were at  $8 \times 10^5$  or better. Antibodies are isolated from the antisera using using conventional techniques, such as immunogen peptide affinity columns. Monoclonal antibodies reactive to *S. cerevisiae* TRT polynucleotide are generated using standard techniques, as discussed above.

#### **Example 20: Design and Construction of Vectors for Expression of TRT Peptides and Polynucleotides**

This example details the design of TRT-expressing bacterial and eukaryotic cell expression vectors to produce large quantities of full-length, biologically active TRTs. Generation of biologically active TRT protein in this manner is useful for telomerase



reconstitution assays, assaying for telomerase activity modulators, analysis of the activity of newly isolated species of TRT, identifying and isolating compounds which specifically associate with TRT, analysis of the activity of an TRT variant protein that has been site-specifically mutated, and as an immunogen, as a few examples.

5

### ***Expression of TRT in Bacteria***

#### **pThioHis A/hTRT Bacterial Expression Vector**

To produce large quantities of full-length TRT, the bacterial expression vector pThioHis A (Invitrogen, San Diego, CA) was selected as an expression system. The  
 10 hTRT-coding insert includes nucleotides 707 to 4776 of the hTRT insert (SEQ ID NO:117) in the plasmid pGRN121. This nucleotide sequence includes the complete coding sequence for the hTRT protein.

This expression vector of the invention is designed for inducible expression in bacteria. The vector can be induced to express, in *E. coli*, high levels of a fusion  
 15 protein composed of a cleavable, HIS tagged thioredoxin moiety and the full length hTRT protein. The use of the expression system was in substantial accordance with the manufacturer's instructions. The amino acid sequence of the fusion protein encoded by the resulting vector of the invention is shown below; (-\*-) denotes an enterokinase cleavage site (SEQ ID NO:130):

20 MSDKIIHLTDDSFDTDLKADGAILVDFWAHWCGPCKMIAPILDEIADEYQGK  
 LTVAKLRIDHNP GTAPKYGIRGIPTLLL FKNGEVAATKVGALSKGQLKEFLDAN  
 LAGSGSGDDDDK-\*--VPMHELEIFEFAAASTQRCVLLRTWEALAPATPAMP RAP  
 RCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVC  
 VPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARG  
 25 GPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGDDVLVHLLARCALFVLV  
 APSCA YQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPL  
 GLPAPGARRRGGSASRSLPLKPRRGAAPEPERTPVGQGSWAHPGRTRGPSD  
 RGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPC  
 PPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTP  
 30 RRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAR

EKPQGSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS  
 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPA  
 EHRLREEILAKFLHWLMSVYVVELLRSSFFYVTETTFQKNRLFFYRKS  
 VWSKLQ  
 SIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRP  
 IVNMDYVV  
 5 GARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDI  
 HRAWRTF  
 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTY  
 CVRRYAVV  
 QKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQ  
 SSSLNE  
 ASSGLFDVFLRFMCHHAVRI  
 RGKSYVQCQGIPQGSILSTLLCSLCYGD  
 MENKLF  
 AGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL  
 RKTVVNF  
 10 PVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTS  
 IRASLTF  
 NRGFKAGRNMRRKLF  
 GVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFH  
 ACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGA  
 AGPLP  
 SEAVQWLCHQAFLKLTRHRVTYVPLLGSLRTAQTQLSRKLP  
 GTTLTALEAAA  
 NPALPSDFKTILD

15

#### **pGEX-2TK with hTRT Nucleotides 3272 to 4177 of pGRN121**

This construct of the invention is used to produce fusion protein for, e.g., the  
 purpose of raising polyclonal and monoclonal antibodies to TRT protein. Fragments of  
 TRT can also be used for other purposes, such as to modulate telomerase activity, for  
 20 example, as a dominant-negative mutant or to prevent the association of a telomerase  
 component with other proteins or nucleic acids.

To produce large quantities of a TRT protein fragment, the *E. coli* expression  
 vector pGEX-2TK (Pharmacia Biotech, Piscataway N.J.) was selected, and used  
 essentially according to manufacturer's instructions to make an expression vector of the  
 25 invention. The resulting construct contains an insert derived from nucleotides 3272 to  
 4177 of the hTRT insert (SEQ ID NO:117) in the plasmid pGRN121. The vector  
 directs expression in *E. coli* of high levels of a fusion protein composed of  
 glutathione-S-transferase sequence (underlined below), thrombin cleavage sequence  
 (double underlined), recognition sequence for heart muscle protein kinase (italicized),

residues introduced by cloning in brackets ([GSVTK]) and hTRT protein fragment (in bold) as shown below (SEQ ID NO:131):

MSPILGYWKIKGLVOPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP  
 NLPYYIDGDVKLTOSMAIRYIADKHNMLGGCPKERAIEISMLEGAVLDIRYGVS  
 5 RIAYSKDFETLKVDLFLSKLPEMLKMEEDRLCHKTYLNGDHVTHPDFMLYDAL  
 DVVLYMDPMCLDAEPKLVCEKKRIEAIPOIDKYLKSSKYIAWPLOGWOATEGG  
 GDHPPKSDLVPRGSRRAST[GSVTK]IPQGSILSTLLCSLCYGD MENKLFAGIR  
 RDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNF  
 10 VEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASV  
 TFNRGFKAGRNMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQ  
 AYRFHACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGA  
 KGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKL  
 PGTTLTALEAAANPALPSDFKTILD

15 When this fusion protein was expressed, it formed insoluble aggregates. It was  
 treated generally as described above, in the section entitled purification of proteins from  
 inclusion bodies. Specifically, induced cells were suspended in PBS (20 mM sodium  
 phosphate, pH 7.4, 150 mM NaCl) and disrupted by sonication. NP-40 was added to  
 0.1%, and the mixture was incubated for 30 minutes at 4°C with gentle mixing. The  
 20 insoluble material was collected by centrifugation at 25,000g for 30 minutes at 4°C.  
 The insoluble material was washed once in 4M urea in PBS, collected by  
 centrifugation, then washed again in PBS. The collected pellet was estimated to  
 contain greater than 75% fusion protein. This material was dried in a speed vacuum,  
 then suspended in adjuvant for injection into mice and rabbits for the generation of  
 25 antibodies.

#### **pGEX-2TK with hTRT Nucleotides 2426 to 3274 of pGRN121 with HIS-8 Tag**

To produce large quantities of a fragment of TRT, another *E. coli* expression  
 vector pGEX-2TK construct was prepared. This construct contains an insert derived  
 30 from nucleotides 2426 to 3274 of the hTRT insert (SEQ ID NO:117) in the plasmid  
 pGRN121 and a sequence encoding eight consecutive histidine residues (HIS-8 Tag).  
 To insert the HIS-8 TAG, the pGEX-2TK vector with hTRT nucleotides 2426 to 3274  
 of pGRN121 was linearized with BamH1. This opened the plasmid at the junction  
 between the GST-thrombin-heart muscle protein kinase and the hTRT coding sequence.

A double stranded oligonucleotide with BamHI compatible ends was ligated to the linearized plasmid resulting in the in-frame introduction of eight histidine residues upstream of the hTRT sequence.

The vector directs expression in *E. coli* of high levels of a fusion protein composed of glutathione-S-transferase sequence (underlined); thrombin cleavage sequence (double underlined); recognition sequence for heart muscle protein kinase (italicized); a set of three and a set of five residues introduced by cloning are in brackets ([GSV] and [GSVTK]); eight consecutive histidines (also double underlined); and hTRT protein fragment (in bold) (SEQ ID NO:132):

10 MSPILGYWKIKGLVOPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP  
NLPYYIDGDVKLTOSMAIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVS  
RIAYSKDEETLKVDELSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL  
DVVLYMDPMCLDAFPKLYCEKKRIEAIPOIDKYLKSSKYIAWPLOGWOATFEGG  
GDHPPKSDLVPRGSRRASV[GSV]HHHHHHHH[GSVTK]MSVYVVELLRSFFYV  
15 TETTFQKNRLFFYRPSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARP  
ALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVL  
NYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTG  
AYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTL  
20 TDLPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHA  
VRIRGKSYVQCQGI

Each of the pGEX-2TK vectors of the invention can be used to produce fusion protein for the purpose of raising polyclonal and monoclonal antibodies to hTRT protein. Additionally, this fusion protein can be used to affinity purify antibodies  
25 raised to TRT peptides that are encompassed within the fusion protein. Separation of the recombinant protein from the glutathione S-transferase moiety can be accomplished by site-specific proteolysis using thrombin according to manufacturer's instructions.

#### **pGEX-2TK with hTRT Nucleotides 2426 to 3274 of pGRN121, no HIS-8 Tag**

30 To produce large quantities of a fragment of TRT, another *E. coli* expression vector pGEX-2TK construct was prepared.

This construct contains an insert derived from nucleotides 2426 to 3274 of the hTRT insert (SEQ ID NO:117) in the plasmid pGRN121, but without the HIS-8 tag of the construct described above. The vector directs expression in *E. coli* of high levels of

a fusion protein composed of glutathione-S-transferase (underlined), thrombin cleavage sequence (double underlined), recognition sequence for heart muscle protein kinase (*italicized*), residues introduced by cloning in brackets ([GSVTK]) and hTRT protein fragment (in bold) (SEQ ID NO:133):

5 MSPILGYWKIKGLVOPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEEP  
NLPYYIDGDVKLTOSMAIRYIADKHNMLGGCPKERAESMLEGAVLDIRYGVS  
RIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL  
DVVLVMDPMCLDAEPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWOATEGG  
GDHPPKSDLVPRGSRRASV[GSVTK]**MSVYVVELLRSFFYVTETTFQKNRLFF**  
 10 **YRPSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPK**  
**PDGLRPIVNMDYVVGARTFRREKRAERLTSRKALFSVLNYERARRPGLLG**  
**ASVLGLDDIHRAWRTFVLRVRAQDPPEYFVKVDVTGAYDTIPQDRLTEVI**  
**ASIIKPQNTYCVRRYAVVQKAAHGVRKAFKSHVSTLTDLQPYMRQFVAHL**  
**QETSPLRDAVVIEQSSSLNEASGLFDVFLRFMCHHAVRIRGKSYVQCQGI**

15

#### pGEX-2TK with hTRT Nucleotides 1625 to 2458 of pGRN121

To produce large quantities of a fragment of TRT protein, another *E. coli* expression vector pGEX-2TK construct was prepared.

This construct contains an insert derived from nucleotides 1625 to 2458 of the  
 20 hTRT insert (SEQ ID NO:117) in the plasmid pGRN121. The vector directs expression in *E. coli* of high levels of a fusion protein composed of glutathione-S-transferase, (underlined), thrombin cleavage sequence (double underlined), recognition sequence for heart muscle protein kinase (*italicized*) residues introduced by cloning in brackets ([GSVTK]) and hTRT protein fragment (in bold) (SEQ ID NO:134):

25 MSPILGYWKIKGLVOPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEEP  
NLPYYIDGDVKLTOSMAIRYIADKHNMLGGCPKERAESMLEGAVLDIRYGVS  
RIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL  
DVVLVMDPMCLDAEPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWOATEGG  
GDHPPKSDLVPRGSRRASV[GSVTK]**ATSLEGALSGTRHSHPSVGRQHHA**  
 30 **STSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL**  
**VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLL**  
**KTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRLVQLLRQHSSPW**  
**QVYGFVRACLRRLVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQELT**  
**WKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELL**  
 35 **RS**

**pGEX-2TK with hTRT Nucleotides 782 to 1636 of pGRN121**

To produce large quantities of a fragment of TRT protein, another *E. coli* expression vector pGEX-2TK construct was prepared.

This construct contains an insert derived from nucleotides 782 to 1636 of the hTRT insert (SEQ ID NO:117) in the plasmid pGRN121. The vector directs expression in *E. coli* of high levels of a fusion protein composed of glutathione-S-transferase, (underlined), thrombin cleavage sequence (double underlined), recognition sequence for heart muscle protein kinase (italicized) residues introduced by cloning in brackets ([GSVTK]) and hTRT protein fragment (in bold) (SEQ ID NO:135):

10 **MSPILGYWKIKGLVOPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP**  
**NLPYYIDGDVKLTOSMAIRYIADKHNLGGCPKERAIEISMLEGAVLDIRYGVS**  
**RIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDEFMLYDAL**  
**DVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWOATFGG**  
**GDHPPKSDLVPRGSRRAISV[GSVTK]MPRAPRCRAVRSLLSHYREVLPLATFV**  
15 **RRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDARPPAAPSFQRQVSC**  
**ELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEATTSVRSYLPNTVTD**  
**ALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPCAYQVCPPPLYQLG**  
**AATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSAS**  
**RSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVS**  
20 **PARPA**  
**EEATSL**

**pT7FLhTRT with hTRT cDNA Lacking 5'-Non-Coding Sequence**

As described above, in one embodiment, the invention provides for an TRT that is modified in a site-specific manner to facilitate cloning into bacterial, mammalian, yeast and insect expression vectors without any 5' untranslated TRT sequence. In some circumstances, minimizing the amount of non-protein encoding sequence allows for improved protein production (yield) and increased mRNA stability. In this embodiment of the invention, the TRT gene's 5' non-coding region was removed before cloning into a bacterial expression vector.

30 This was effected by engineering an additional restriction endonuclease site just upstream (5') to the start (ATG) codon of the hTRT coding sequence (Figure 53, SEQ ID NO:117). The creation of a restriction site just 5' to the coding region of the protein allows for efficient production of a wide variety of vectors that encode fusion proteins.

such as fusion proteins comprising labels and peptide TAGs, for immunodetection and purification.

Specifically, the oligonucleotide 5'-

CCGGCCACCCCCCATATGCCGCGCGCTCCC-3' (SEQ ID NO:136) was used as

5 described above to modify hTRT cDNA nucleotides 779 to 781 of the hTRT cDNA (SEQ ID NO:117) from GCG to CAT. These 3 nucleotides are the last nucleotides before the ATG start codon so they do not modify the protein sequence. The change in sequence results in the creation of a unique NdeI restriction site in the hTRT cDNA.

Single-stranded hTRT DNA was used as a DNA source for the site directed  
10 mutagenesis. The resulting plasmid was sequenced to confirm the success of the mutagenesis.

This modification allowed the construction of the following plasmid of the invention, designated pT7FLhTRT. The site-specifically modified hTRT sequence (addition of the NdeI restriction site) was digested with NdeI and NotI (and filled in  
15 with Klenow fragment to generate a blunt ended DNA) to generate an hTRT encoding nucleic acid fragment. The fragment was then cloned into a pSL3418 plasmid previously restriction digested with NdeI and SmaI (also a blunt ended cutter). pSL 3418 is a modified pAED4 plasmid into which a FLAG sequence (Immunex Corp, Seattle WA) and an enterokinase sequence are inserted just upstream from the above-  
20 referenced NdeI site. This plasmid, designated pT7FLhTR, allows the expression of full length hTRT (with a Flag-Tag at its 5' end) in an *E.coli* strain expressing the T7 RNA polymerase.

#### **Plasmids with hTRT cDNA Lacking 3'-Non-Coding Sequence**

25 As discussed above, the invention provides for expression vectors containing TRT-encoding nucleic acids in which some or all non-coding sequences have been deleted. In some circumstances, minimizing the amount of non-protein encoding sequence allows for improved protein production (yield) and increases mRNA stability. In this embodiment of the invention, the 3' untranslated region of TRT is deleted before cloning into a bacterial  
30 expression plasmid.

The plasmid pGRN121, containing the full length hTRT cDNA, as discussed above, was first deleted of all ApaI sites. This was followed by deletion of the MscI-HincII hTRT restriction digest enzyme fragment containing the 3'UTR. The NcoI-XbaI restriction digest fragment containing the stop codon of hTRT was then inserted  
5 into the NcoI-XbaI site of pGRN121, designated pGRN124, except lacking the 3'UTR.

#### Bacterial Expression Vectors Using Antibiotic Selection Markers

The invention also provides for bacterial expression vectors that can contain selection markers to confer a selectable phenotype on transformed cells and sequences  
10 coding for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance, particularly resistance to chloramphenicol (see Harrod (1997) *Nucleic Acids Res.* 25: 1720-1726), kanamycin, G418, bleomycin and hygromycin, to permit selection of those cells transformed with the desired DNA sequences, see for example, Blondelet-Rouault (1997)  
15 Gene 190:315-317; and Mahan (1995) *Proc Natl Acad Sci U S A* 92:669-673.

In one embodiment of the invention, the full length hTRT was cloned into a modified BlueScript plasmid vector (Stratagene, San Diego, CA), designated pBBS235, into which a chloramphenicol antibiotic resistance gene had been inserted. The NotI fragment from pGRN124 (discussed above) containing the hTRT ORF into the NotI site  
20 of pBBS235 so that the TRT ORF is in the opposite orientation of the vector's Lac promoter. This makes a plasmid that is suitable for mutagenesis of plasmid inserts, such as TRT nucleic acids of the invention. This plasmid construct, designated pGRN125, can be used in the methods of the invention involving mutagenesis of telomerase enzyme and TRT protein coding sequences and for *in vitro* transcription of hTRT using the T7  
25 promoter (and *in vitro* transcription of antisense hTRT using the T3 promoter).

In another embodiment of the invention, NotI restriction digest fragments from pGRN124 containing the hTRT ORF were subcloned into the NotI site of pBBS235 (described above) so the TRT ORF is in the same orientation as the vector's Lac promoter. This makes a plasmid, designated pGRN126, that can be used for expression of full length  
30 hTRT in *E. coli*. The expressed product will contain 29 amino acids encoded by the vector



pBBS235, followed by 18 amino acids encoded by the 5'UTR of hTRT, followed by the full length hTRT protein.

In a further embodiment of the invention, *in vitro* mutagenesis of pGRN125 was done to convert the hTRT initiating ATG codon into a Kozak consensus and create EcoRI and BglII restriction digest sites to facilitate cloning into expression vectors. The oligonucleotide 5'-TGCGCACGTGGGAAGCCCTGGCagatctgAatt CcaCcATGCCGCGCGCTCCCCGCTG-3' (altered nucleotides in lower case) (SEQ ID NO:137) was used in the mutagenesis procedure. The resulting expression vector was designated pGRN127.

In another embodiment of the invention, the second Asp of the TRT "DD motif" was converted to an alanine to create a non-functional telomerase enzyme, thus creating a mutant TRT protein for use as a dominant/negative mutant. The hTRT coding sequence was mutagenized *in vitro* using the oligonucleotide 5'-CGGGACGGGCTGCTCCTGCGTTTGGTGGAcGcgTTCTTGTTGGTGACACCTCA CCTCACC-3' (SEQ ID NO:138) to convert the asparagine codon for residue 869 (Asp869) to an alanine (Ala) codon. This also created an MluI restriction enzyme site. The resulting expression plasmid was designated GRN130, which also contains the Kozak consensus sequence as described for pGRN127.

In another embodiment of the invention, oligonucleotide 5'-TGCGCACGTGGGAAGCCCTGGCagatctgAattCCaCcATGCCGCGCGCTCCCCGCTG-3' (SEQ ID NO:139) was used in an *in vitro* mutagenesis procedure to convert the hTRT initiating ATG codon into a Kozak consensus sequence and to create EcoRI and BglII restriction sites for cloning.

The invention also provides a vector designed to express an antisense sequence fragment of hTRT. The pGRN126 plasmid was cut to completion with MscI and SmaI restriction enzymes and religated to delete over 95% of the hTRT ORF. One SmaI-MscI fragment was re-inserted during the process to recreate CAT activity. This unpurified plasmid was then redigested with SalI and EcoRI and the fragment containing the initiating codon of the hTRT ORF was inserted into the SalI-EcoRI sites of pBBS212 to make an

antisense expression plasmid expressing the antisense sequence spanning the 5'UTR and 73 bases pair residues of the hTERT ORF. This plasmid was designated pGRN135.

***Expression of hTERT Telomerase in Yeast***

- 5           The present invention also provides TRT-expressing yeast expression vectors to produce large quantities of full-length, biologically active TRT.

**Pichia pastoris Expression Vector pPICZ B and Full Length hTERT**

- 10           To produce large quantities of full-length, biologically active TRT, the *Pichia pastoris* expression vector pPICZ B (Invitrogen, San Diego, CA) was selected. The hTERT-coding sequence insert was derived from nucleotides 659 to 4801 of the hTERT insert (SEQ ID NO:117) in plasmid pGRN121. This nucleotide sequence includes the full-length sequence encoding hTERT. This expression vector is designed for inducible expression in *P. pastoris* of high levels of full-length, unmodified hTERT protein. Expression is driven  
15   by a yeast promoter, but the expressed sequence utilizes the hTERT initiation and termination codons. No exogenous codons were introduced by the cloning. The resulting pPICZ B/hTERT vector was used to transform the yeast.

**Pichia pastoris Expression Vector hTRT-His6/pPICZ B**

A second *Pichia pastoris* expression vector of the invention derived from pPICZ B, also contains the full-length sequence encoding hTRT derived from nucleotides 659 to 4801 of the hTRT insert (SEQ ID NO:117) in the plasmid pGRN121. This

5 hTRT-His6/pPICZ B expression vector encodes full length hTRT protein fused at its C-terminus to the Myc epitope and His6 reporter tag sequences. The hTRT stop codon has been removed and replaced by vector sequences encoding the Myc epitope and the His6 reporter tag as well as a stop codon. This vector is designed to direct high-level inducible expression in yeast of the following fusion protein, which consists of hTRT sequence

10 (underlined), vector sequences in brackets ([L] and [NSAVD]) the Myc epitope (double underlined), and the His6 tag (italicized) (SEQ ID NO:140):

MPRAPRCRAVRSLLRSHYREVLPLATEFVRRRLGPOGWRLVORGDPAAFRALVA  
OCLVCVPWDARPPPAAPSFROVSKELVARVLORLCERGAKNVLAFGFALL  
DGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARC  
15 ALFVLVAPSCAYOVCGPPLYOLGAATOARPPPHASGPRRRRLGCERAWNHSVR  
EAGVPLGLPAPGARRRGGSASRSLPLKPRRRGAAPERTPVGOGSWAHPGR  
TRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGROHHAGPPSTSRPPR  
PWDTPCPPVYAETKHFYSSGDKEOLRPSSELLSLRPSLTGARRLVETIFLGSRP  
WMPGTPRRLPRLPORYWOMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPA  
20 AGVCAREKPOGSVAAPEEEDTDPRRLVOLLROHSSPWQVYGEVRACLRRLVP  
PGLWGSRHNERRELNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGV  
GCVPAAEHRLREEILAKELHWLMSVYVVELLRSEFFVTETTEOKNRLEFFYRKS  
VWSKLOSIGIROHLKRVOLRELSAEVROHREARPALLTSRLRFIPKPDGLRPV  
NMDYVVGARTERREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIH  
25 RAWRTFVLRVRAODPPPELYFVKVDVTGAYDTIPODRLTEVIASIIKPONTYCV  
RRYAVVOKAAHGHVRKA EKSHVSTLTDLOPYMROFVAHLOETSPLRDAVVIE  
QSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVOCOGIPOGSILSTLLCSLCYGD  
MENKLFAGIRRDGLLLRLVDDELLVTPHLTHAKTELRTLYRGVPEYGCVVNLR  
KTVVNFPEDEALGGTAFAVOMPAHGLEFPWCGLLLDTRTLEVQSDYSSYARTSI  
30 RASLTENRGEKAGRNMRKLEGVRLKCHSLFELDLOVNSLOTVCCTNIYKILLLO  
AYREHACVLOLPEHOQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGA  
AGPLPSEAVQWLCHOAFLKLTRHRVTYVPLLGLSLRTAOTOLSRKLP GTTLTA  
LEAAANPALPSDEKTILD[L]EOKLISEEDL[NSAVD]HHHHHH

35 Separation of the recombinant protein from the glutathione S-transferase moiety is accomplished by site-specific proteolysis using thrombin according to manufacturer's instructions.

### Expression of TRT in Insect Cells

The present invention also provides TRT telomerase-expressing insect cell expression vectors that produce large quantities of full-length, biologically active TRT.

#### 5 Baculovirus Expression Vector pVL1393 and Full Length TRT

The TRT coding sequence of interest was cloned into the baculovirus expression vector pVL1393 (Invitrogen, San Diego, CA). This construct was subsequently cotransfected into *Spodoptera frugiperda* (sf-9) cells with linearized DNA from *Autographa californica* nuclear polyhedrosis virus (Baculogold-AcMNPV). The recombinant  
10 baculoviruses obtained were subsequently plaque purified and expanded following standard protocols.

This expression vector provides for expression in insect cells of high levels of full-length TRT protein. Expression is driven by a baculoviral polyhedrin gene promoter. No exogenous codons were introduced by the cloning.

15

#### Baculovirus Expression Vector pBlueBacHis2 B and Full Length hTRT

To produce large quantities of full-length, biologically active TRT, the baculovirus expression vector pBlueBacHis2 B (Invitrogen, San Diego, CA) was selected as a source of control elements. The hTRT-coding insert consisted of nucleotides 707 to 4776 of the  
20 hTRT insert (SEQ ID NO:117) in plasmid pGRN121.

A full length hTRT with a His6 and Anti-Xpress tags (Invitrogen) was also constructed. This vector also contains an insert consisting of nucleotides 707 to 4776 of the hTRT insert from the plasmid pGRN121. The vector directs expression in insect cells of high levels of full length hTRT protein fused to a cleavable 6-histidine and Anti-Xpress  
25 tags, and the amino acid sequence of the fusion protein is shown below; (-\*-) denotes enterokinase cleavage site (SEQ ID NO:141):

MPRGSHHHHHHGMASMTGGQQMGRDLYDDDDL-\*DPSSRSAAGTMEFAAA  
STQRCVLLRTWEALAPATPAMPRAVRSLLRSHYREVLPLATFVRRLLGP  
QGWRLVQRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVL  
30 QRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAW  
GLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPPH

ASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGA  
 APEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHS  
 HPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSS  
 LRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQ  
 5 CPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQH  
 SSPWQVYGFVRACLRRLLVPPGLWGRHNERRFLRNTKKFISLGKHAKLSLQEL  
 TWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLSF  
 FYVTETTFQKNRLFFYRKSWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARP  
 ALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNVE  
 10 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIP  
 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMR  
 QFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQC  
 QGIPQGSILSTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTF  
 LRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLL  
 15 DTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFVLRLLKCHSLFLDL  
 QVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQVWKNPTFFLRVISDTASLC  
 YSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLKLTRHRVTYVPLLGS  
 LRTAQTQLSRKLP GTTLTALEAAANPALPSDFKTILD

#### 20 **Baculovirus Expression Vector pBlueBac4.5 and Full Length hTRT Protein**

To produce large quantities of full-length, biologically active TRT, a second  
 baculovirus expression vector, pBlueBac4.5 (Invitrogen, San Diego, CA) was constructed.  
 The hTRT-coding insert also consisted of nucleotides 707 to 4776 of the hTRT (SEQ ID  
 NO:117) from the plasmid pGRN121.

25

#### **Baculovirus Expression Vector pMelBacB and Full Length TRT Protein**

To produce large quantities of full-length, biologically active TRT, a third  
 baculovirus expression vector, pMelBacB (Invitrogen, San Diego, CA) was constructed.  
 The hTRT-coding insert also consists of nucleotides 707 to 4776 of the hTRT insert from  
 30 the plasmid pGRN121.

pMelBacB directs expression of full length TRT in insect cells to the  
 extracellular medium through the secretory pathway using the melittin signal sequence.  
 High levels full length TRT are thus secreted. The melittin signal sequence is cleaved  
 upon excretion, but is part of the protein pool that remains intracellularly. For that reason,  
 35 it is indicated in parentheses in the following sequence. The sequence of the fusion protein  
 encoded by the vector is shown below (SEQ ID NO:142):

(MKFLVNVALVFMVVYISYIYA)-\*-DPSSRSAAGTMEFAAASTQRCVLLRTWE  
 ALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRVLRQGRDP  
 AAFRALVAQCLVCVPWDARPPPAAPSFQVSCLELVARVLQRLCERGAKNV  
 LAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGGDVL  
 5 VHLLARCALFVLVAPSCAYQVCGPLYQLGAATQARPPPHASGPRRRLGCERA  
 WNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGS  
 WAHPGRTRGPSDRGFCVVSAPPAEEATSLEGALSGTRHSHPSVGRQHHAGPP  
 STSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVET  
 IFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLR  
 10 AAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRAC  
 LRRLVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWL  
 RRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLSFFYVTETTFQKNRL  
 FFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPD  
 GLRPVNMMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVL  
 15 GLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKP  
 QNTYCVRRYA VVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLR  
 DAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIQGSILSTLLC  
 SLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYG  
 CVVNLRKTVVNFVVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS  
 20 SYARTSIRASLTFNRGFKAGRNMRRLKFGVLRLKCHSLFLDLQVNSLQTVCTNI  
 YKILLQAYRFHACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMS  
 LGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSRLTAQTQLSRKLP  
 GTTLTALEAAANPALPSDFKTILD

25

### **Expression of TRT in Mammalian Cells**

The present invention also provides vectors to produce TRT in large quantities as full-length, biologically active protein in a variety of mammalian cell lines, which is useful in many embodiments of the invention, as discussed above.

30

### **MPSV-TRT Expression Plasmids**

The invention also provides for an expression system for use in mammalian cells that give the highest possible expression of recombinant protein, such as telomerase, without actually modifying the coding sequence (*e.g.* optimizing codon usage). In one  
 35 embodiment, the invention provides MPSV mammalian expression plasmids (using a system described by Lin J-H (1994) *Gene* 47:287-292) capable of expressing the TRTs of the invention. The MPSV plasmids can be expressed either as stable or transient clones.

In this expression system, while the hTRT coding sequence itself is unchanged, exogenous transcriptional control elements are incorporated into the vector. The myeloproliferative sarcoma virus (MPSV) LTR (MPSV-LTR) promoter, enhanced by the cytomegalovirus (CMV) enhancer, is incorporated for transcriptional initiation. This promoter consistently shows higher expression levels in cell lines (see Lin J-H (1994) *supra*). A Kozak consensus sequence can be incorporated for translation initiation (see Kozak (1996) *Mamm. Genome* 7:563-574). All extraneous 5' and 3' untranslated hTRT sequences can be removed to insure that these sequences do not interfere with expression, as discussed above. The MPSV plasmid containing the complete hTRT coding sequence, but with all extraneous sequences removed, is designated pGRN133. A control, hTRT "antisense" plasmid was also constructed. This vector is identical to pGRN133 except that the TRT insert is the antisense sequence of hTRT (the antisense, which control can be used as a vector is designated pGRN134).

Two selection markers, PAC (Puromycin-N-acetyl-transferase = Puromycin resistance) and HygB (Hygromycin B = Hygromycin resistance) are present for selection of the plasmids after transfection (see discussion referring to selectable markers, above). Double selection using markers on both sides of the vector polylinker should increase the stability of the hTRT coding sequence. A DHFR (dihydrofolate reductase) encoding sequence is included to allow amplification of the expression cassette after stable clones are made. Other means of gene amplification can also be used to increase recombinant protein yields.

The invention also provides for MPSV mammalian expression plasmids containing TRT fusion proteins. In one embodiment, the TRT sequence, while retaining its 5' untranslated region, is linked to an epitope flag, such as the IBI FLAG (International Biotechnologies Inc. (IBI), Kodak, New Haven, CT) and inserted into the MPSV expression plasmid (designated pGRN147). This particular construct contains a Kozak translation initiation site. The expressed fusion protein can be purified using the M-1 anti-FLAG octapeptide monoclonal antibody (IBI, Kodak, *supra*).

In another embodiment, TRT is site-specifically altered. One amino acid residue codon is mutagenized, changing the aspartic acid at position 869 to an alanine. This

Asp869->Ala hTRT mutant, retaining its 5' untranslated region and incorporating a Kozak sequence, was inserted into an MPSV expression plasmid, and designated pGRN146. The Asp869->Ala hTRT mutant was further engineered to contain the FLAG sequence, as described above, and the insert cloned into an MPSV expression plasmid. This expression  
5 plasmid was designated pGRN154. Specifically, for pGRN154, an Eam1105I restriction digest fragment from pGRN146 containing the Kozak sequence-containing "front end" (5' segment) of hTRT was cloned into the Eam1105I sites of pGRN147 (see above) to make an MPSV expression plasmid capable of expressing hTRT with a Kozak sequence, the above-described D869->A mutation, and the IBI flag.

10 Another embodiment of the invention is an expression plasmid derived from pGRN146. The mammalian expression plasmid, designated pGRN152, was generated by excising the EcoRI fragment from plasmid pGRN146 (containing the TRT ORF in mammalian cells) and cloned into the EcoRI site of pBBS212 to remove the 5'UTR of hTRT. The hTRT is oriented so that its expression is controlled by the MPSV promoter.  
15 This makes a mammalian expression plasmid that expresses hTRT with a Kozak consensus sequence and the D869->A mutation, and uses the MPSV promoter.

The invention provides for a mammalian expression vector in which TRT is oriented so that the TRT coding sequence is driven by the MPSV promoter. For example, an EcoRI restriction digest fragment from pGRN137 containing the hTRT open reading  
20 frame (ORF) was cloned into the EcoRI site of pBBS212 (see below), thus removing the 5' untranslated region (5'-UTR) of hTRT. pGRN137 was constructed by excising a Sall-Sse8387I fragment from pGRN130, described below, containing the Kozak mutation of hTRT into the Sal I-SSE 8387I sites of pGRN136, making a mammalian expression plasmid expressing hTRT containing a Kozak consensus sequence off the MPSV promoter.  
25 Plasmid pGRN136 was constructed by excising a HindIII Sall fragment from pGRN126 containing the hTRT ORF and cloning it into the HindIII Sall sites of plasmid, pBBS242, making a mammalian expression plasmid expressing hTRT off the MPSV promoter). This makes a mammalian expression plasmid, designated pGRN145, that expresses hTRT with a Kozak consensus sequence using the MPSV promoter. See also the pGRN152  
30 MPSV promoter-driven mammalian expression vector described below.



**TRT Expressed in 293 Cells using Episomal Vector pEBVHis**

An episomal vector, pEBVHis (Invitrogen, San Diego, CA) was engineered to express an TRT fusion protein comprising hTRT fused to an N-terminal extension epitope tag, the Xpress epitope (Invitrogen, San Diego, CA) (designated pGRN122). The NotI hTRT fragment from pGRN121 containing the hTRT ORF was cloned into the NotI site of pEBVHisA so that the hTRT ORF is in the same orientation as the vector's Rous Sarcoma Virus (RSV) promoter. In this orientation the His6 flag was relatively closer to the N-terminus of hTRT.

A vector was also constructed containing as an insert the antisense sequence of TRT and the epitope tag (the plasmid designated pGRN123, which can be used as a control). The vector was transfected into 293 cells and translated hTRT identified and isolated using an antibody specific for the Xpress epitope. pEBVHis is a hygromycin resistant EBV episomal vector that expresses the protein of interest fused to a N-terminal peptide. Cells carrying the vector are selected and expanded, then nuclear and cytoplasmic extracts prepared. These and control extracts are immunoprecipitated with anti-Xpress antibody, and the immunoprecipitated beads are tested for telomerase activity by conventional assay.

**Expression Recombinant TRT in Mortal, Normal Diploid Human Cells**

In one embodiment of the invention, recombinant TRT and necessary telomerase enzyme complex components can be expressed in normal, diploid mortal cells to increase their proliferative capacity or to immortalize them, or to facilitate immortalizing them. This allows one to obtain diploid immortal cells with an otherwise normal phenotype and karyotype. As discussed above, this use of telomerase has enormous commercial utility.

Sense hTRT (Figure 16) and antisense hTRT) were cloned into a CMV vector. These vectors were purified and transiently transfected into two normal, mortal, diploid human cell clones. The human clones were young passage diploid human BJ and IMR90 cell strains.

Analysis of telomerase activity using a TRAP assay (utilizing the TRAPeze™ Kit (Oncor, Inc., Gaithersburg, MD) showed that transfection of sense hTERT - but not antisense hTERT - generated telomerase activity in both the BJ and IMR90 cell strains.

5     **Expression of Recombinant TRT in Immortalized IMR90 Human Cells**

Using the same TRT sense construct cloned into CMV vectors used in the above described diploid human BJ and IMR90 cell strains studies, immortalized SW13 ALT pathway cell line (an IMR90 cell immortalized with SV40 antigen) was transiently transfected. A TRAP assay (TRAPeze, Oncor, Inc, Gaithersburg, MD) demonstrated that  
10     telomerase activity was generated in the sense construct transfected cells.

**Vectors for Regulated Expression of hTERT in Mammalian Cells: Inducible and Repressible Expression of hTERT**

The invention provides vectors that can be manipulated to induce or repress the  
15     expression of the TRTs of the invention, such as hTERT. For example, the hTERT coding sequence can be cloned into the Ecdysone-Inducible Expression System from Invitrogen (San Diego, CA) and the Tet-On and Tet-off tetracycline regulated systems from Clontech Laboratories, Inc. (Palo Alto, CA). Such inducible expression systems are provided for use in the methods of the invention where it is important to control the level or rate of  
20     transcription of transfected TRT. For example, the invention provides for cell lines immortalized through the expression of TRT; such cells can be rendered "mortal" by inhibition of TRT expression by the vector through transcriptional controls, such as those provided by the Tet-Off system. The invention also provides for methods of expressing TRT only transiently to avoid the constitutive expression of TRT, which may lead to  
25     unwanted "immortalization" of the transfected cells, as discussed above.

The Ecdysone-Inducible Mammalian Expression System is designed to allow regulated expression of the gene of interest in mammalian cells. The system is distinguished by its tightly regulated mechanism that allows almost no detectable basal expression and greater than 200-fold inducibility in mammalian cells. The expression  
30     system is based on the heterodimeric ecdysone receptor of *Drosophila*. The

Ecdysone-Inducible Expression System uses a steroid hormone ecdysone analog, muristerone A, to activate expression of TRT via a heterodimeric nuclear receptor. Expression levels have been reported to exceed 200-fold over basal levels with no effect on mammalian cell physiology "Ecdysone-Inducible Gene Expression in Mammalian Cells and Transgenic Mice" (1996) *Proc. Natl. Acad. Sci. USA* 93, 3346-3351). Once the receptor binds ecdysone or muristerone, an analog of ecdysone, the receptor activates an ecdysone-responsive promoter to give controlled expression of the gene of interest. In the Ecdysone-Inducible Mammalian Expression System, both monomers of the heterodimeric receptor are constitutively expressed from the same vector, pVgRXR. The ecdysone-responsive promoter, which ultimately drives expression of the gene of interest, is located on a second vector, pIND, which drives the transcription of the gene of interest.

The TRT coding sequence is cloned in the pIND vector (Clontech Laboratories, Inc, Palo Alto, CA), which contains 5 modified ecdysone response elements (E/GREs) upstream of a minimal heat shock promoter and the multiple cloning site. The construct is then transfected in cell lines which have been pre-engineered to stably express the ecdysone receptor. After transfection, cells are treated with muristerone A to induce intracellular expression from pIND.

The Tet-on and Tet-off expression systems (Clontech, Palo Alto, CA) give access to the regulated, high-level gene expression systems described by Gossen (1992) "Tight control of gene expression in mammalian cells by tetracycline responsive promoters" *Proc. Natl. Acad. Sci. USA* 89:5547-5551, for the Tet-Off transcription repression system; and Gossen (1995) "Transcriptional activation by tetracycline in mammalian cells" *Science* 268:1766-1769, for the Tet-On inducible transcriptional system. In "Tet-Off" transformed cell lines, gene expression is turned on when tetracycline (Tc) or doxycycline ("Dox," a Tc derivative) is removed from the culture medium. In contrast, expression is turned on in Tet-On cell lines by the addition of Tc or Dox to the medium. Both systems permit expression of cloned genes to be regulated closely in response to varying concentrations of Tc or Dox.

This system uses the "pTRE" as a response plasmid that can be used to express a gene of interest. Plasmid pTRE contains a multiple cloning site (MCS) immediately

downstream of the Tet-responsive PhCMV\*-1 promoter. Genes or cDNAs of interest inserted into one of the sites in the MCS will be responsive to the tTA and rTA regulatory proteins in the Tet-Off and Tet-On systems, respectively. PhCMV\*-1 contains the Tet-responsive element (TRE), which consists of seven copies of the 42-bp tet operator sequence (tetO). The TRE element is just upstream of the minimal CMV promoter (PminCMV), which lacks the enhancer that is part of the complete CMV promoter in the pTet plasmids. Consequently, PhCMV\*-1 is silent in the absence of binding of regulatory proteins to the tetO sequences. The cloned insert must have an initiation codon. In some cases, addition of a Kozak consensus ribosome binding site may improve expression levels; however, many cDNAs have been efficiently expressed in Tet systems without the addition of a Kozak sequence. pTRE-Gene X plasmids are cotransfected with pTK-Hyg to permit selection of stable transfectants.

Setting up a Tet-Off or Tet-On expression system generally requires two consecutive stable transfections to create a "double-stable" cell line that contains integrated copies of genes encoding the appropriate regulatory protein and TRT under the control of a TRE. In the first transfection, the appropriate regulatory protein is introduced into the cell line of choice by transfection of a "regulator plasmid" such as pTet-Off or pTet-On vector, which expresses the appropriate regulatory proteins. The hTRT cloned in the pTRE "response plasmid" is then introduced in the second transfection to create the double-stable Tet-Off or Tet-On cell line. Both systems give very tight on/off control of gene expression, regulated dose-dependent induction, and high absolute levels of gene expression.

#### **Expression Recombinant TRT With DHFR and Adenovirus Sequences**

The pGRN155 plasmid construct was designed for transient expression of hTRT cDNA in mammalian cells. A Kozak consensus is inserted at the 5' end of the hTRT sequence. The hTRT insert contains no 3' or 5' UTR. The hTRT cDNA is inserted into the EcoRI site of p91023(B) (Wong (1985) *Science* 228:810-815). The hTRT insert is in the same orientation as the DHFR ORF. This makes the expression vector particularly useful for transient expression.

Plasmid pGRN155 contains the SV40 origin and enhancer just upstream of an adenovirus promoter, a tetracycline resistance gene, an *E. coli* origin and an adenovirus VAI and VAI gene region. This expression cassette contains, in the following order: the adenovirus major late promoter; the adenovirus tripartite leader; a hybrid intron consisting  
5 of a 5' splice site from the first exon of the tripartite leader and a 3' splice site from the mouse immunoglobulin gene; the hTRT cDNA; the mouse DHFR coding sequence; and, the SV40 polyadenylation signal.

The adenovirus tripartite leader and the VA RNAs have been reported to increase the efficiency with which polycistronic mRNAs are translated. DHFR sequences have  
10 been reported to enhance the stability of hybrid mRNA. DHFR sequences also can provide a marker for selection and amplification of vector sequences. See Logan (1984) *Proc. Natl. Acad. Sci. USA* 81:3655; Kaufman (1985) *Proc. Natl. Acad. Sci. USA* 82: 689 ; and Kaufman (1988) *Focus* (Life Technologies, Inc.), Vol.10, no. 3).

**Other expression plasmids of the invention are described for illustrative  
15 purposes.**

**pGRN121**

The EcoRI fragment from lambda clone 25-1.1.6 containing the entire cDNA encoding hTRT protein was inserted into the EcoRI site of pBluescriptII SK+ such that the 5' end of the cDNA is near the T7 promoter in the vector. The selectable marker that is used with  
20 this vector is ampicillin.

**pGRN122**

The NotI fragment from pGRN121 containing the hTRT ORF was inserted into the NotI site of pEBVHisA so that the coding sequence is operably linked to the RSV promoter. This plasmid expresses a fusion protein composed of a His6 flag fused to the N-terminal  
25 of the hTRT protein. The selectable marker that is used with this vector is ampicillin or hygromycin.

**pGRN123**

The NotI fragment from pGRN121 containing the hTRT ORF was inserted into the NotI site of pEBVHisA so that the coding sequence is in the opposite orientation as the RSV  
30 promoter, thus expressing *antisense* hTRT.

**pGRN124**

Plasmid pGRN121 was deleted of all *ApaI* sites followed by deletion of the *MscI*-*HincII* fragment containing the 3'UTR. The *Nco*-*XbaI* fragment containing the stop codon of the hTERT coding sequence was then inserted into the *Nco*-*XbaI* sites of pGRN121 to make a  
 5 plasmid equivalent to pGRN121 except lacking the 3'UTR, which may be preferred for increased expression levels in some cells.

**pGRN125**

The *NotI* fragment from pGRN124 containing the hTERT coding sequence was inserted into the *NotI* site of pBBS235 so that the open reading frame is in the opposite orientation of  
 10 the Lac promoter. The selectable marker that is used with this vector is chloramphenicol.

**pGRN126**

The *NotI* fragment from pGRN124 containing the hTERT coding sequence was inserted into the *NotI* site of pBBS235 so that the hTERT coding sequence inserted is in the same orientation as the Lac promoter.

**pGRN127**

The oligonucleotide 5'-TGCGCACGTGGGAAGCCCTGGCagatctgAattCCaCcATGC  
 CGCGCGCTCCCCGCTG-3' (SEQ ID NO:143) was used *in vitro* mutagenesis of  
 pGRN125 to convert the initiating ATG codon of the hTERT coding sequence into a Kozak  
 consensus sequence and create *EcoRI* and *BglII* sites for cloning. Also, oligonucleotide  
 20 COD2866 was used to convert AmpS to AmpR (ampicillin resistant) and oligonucleotide  
 COD1941 was used to convert CatR (chloramphenicol resistant) to CatS (chloramphenicol  
 sensitive).

**pGRN128**

The oligonucleotide 5'-TGCGCACGTGGGAAGCCCTGGCagatctgAattCCaCcATG  
 25 CCGCGCGCTCCCCGCTG-3' (SEQ ID NO:144) was used in *in vitro* mutagenesis to  
 convert the initiating ATG codon of hTERT into a Kozak consensus and create *EcoRI* and  
*BglII* sites for cloning.

Also, oligo 5'-CTGCCCTCAGACTTCAAGACCATCCTGGACTACAA  
 GGACGACGATGACAAATGAATTCAGATCTGCGGCCGCCACCGCGGTGGAG  
 30 CTCCAGC-3' (SEQ ID NO:145) was used to insert the IBI Flag (International

Biotchnologies Inc. (IBI), Kodak, New Haven, CT) at the C-terminus and create EcoRI and BglII sites for cloning. Also, COD2866 was used to convert AmpS to AmpR and COD1941 was used to convert CatR to CatS.

**pGRN129**

- 5 The oligonucleotide 5'-CGGGACGGGCTGCTCCTGCGTTTGGTGGAcGcgTTCTTG  
TTGGTGACACCTCACCTCACC-3' (SEQ ID NO:146) was used by *in vitro* mutagenesis  
to convert Asp869 to an Ala codon (i.e. the second Asp of the DD motif was converted to  
an Alanine to create a dominant/negative hTRT mutant). This also created a MluI site.  
Also, oligonucleotide 5'-CTGCCCTCAGACTTCAAGACCATCCTGGACTACAAGG  
10 1.ACGACGATGACAAATGAATTCAGATCTGCGGCCGCCACCGCGGTGGAGCT  
CCAGC-3 (SEQ ID NO:147) was used to insert the IBI Flag at the C-terminus and create  
EcoRI and BglII sites for cloning. Also, COD2866 was used to convert AmpS to AmpR  
and COD1941 was used to convert CatR to CatS.

**pGRN130**

- 15 The oligonucleotide 5'-CGGGACGGGCTGCTCCTGCGTTTGGTGGAcGcgTTCTT  
GTTGGTGACACCTCACCTCACC-3' (SEQ ID NO:148) was used in *in vitro*  
mutagenesis to convert the Asp869 codon into an Ala codon (i.e. the second Asp of the DD  
motif was converted to an Alanine to make a dominant/negative variant protein). This also  
created an MluI site.

- 20 Also, the oligonucleotide 5'-TGCGCACGTGGGAAGCCCTGGCagatctgAatt  
CcaCcATGCCGCGCGCTCCCCGCTG-3' (SEQ ID NO:149) was used in *in vitro*  
mutagenesis to convert the initiating ATG codon of the hTRT coding sequence into a  
Kozak consensus sequence and create EcoRI and BglII sites for cloning. Also, COD2866  
was used to convert AmpS to AmpR and COD1941 was used to convert CatR.

**pGRN131**

25 The EcoRI fragment from pGRN128 containing the hTRT ORF with Kozak sequence and  
IBI Flag mutations is inserted into the EcoRI site of pBBS212 so that the hTRT ORF is  
expressed off the MPSV promoter. Plasmid pBSS212 contains a MPSV promoter, the  
CMV enhancer, and the SV40 polyadenylation site.

**pGRN132**

The EcoRI fragment from pGRN128 containing the hTRT ORF with Kozak sequence and IBI Flag mutations is inserted into the EcoRI site of pBBS212 so that the antisense of the hTRT ORF is expressed off the MPSV promoter.

5 **pGRN133**

The EcoRI fragment from pGRN121 containing the hTRT coding sequence was inserted into the EcoRI site of pBBS212 so that the hTRT protein is expressed under the control of the MPSV promoter.

**pGRN134**

- 10 The EcoRI fragment from pGRN121 containing the hTRT coding sequence was inserted into the EcoRI site of pBBS212 so that the *antisense* of the hTRT coding sequence is expressed under the control of the MPSV promoter. The selectable markers used with this vector are Chlor/HygB/PAC.

**pGRN135**

- 15 Plasmid pGRN126 was digested to completion with MscI and SmaI and religated to delete over 95% of the hTRT coding sequence inserted. One SmaI-MscI fragment was re-inserted during the process to recreate the Cat activity for selection. This unpurified plasmid was then redigested with SalI and EcoRI and the fragment containing the initiating codon of the hTRT coding sequence was inserted into the SalI-EcoRI sites of pBBS212.
- 20 This makes an *antisense* expression plasmid expressing the antisense of the 5'UTR and 73 bases of the coding sequence. The selectable markers used with this vector are Chlor/HygB/PAC.

**pGRN136**

- 25 The HindIII-SalI fragment from pGRN126 containing the hTRT coding sequence was inserted into the HindIII-SalI sites of pBBS242.

**pGRN137**

The SalI-Sse8387I fragment from pGRN130 containing the Kozak sequence was inserted into the SalI-Sse8387I sites of pGRN136.



**pGRN138**

The EcoRI fragment from pGRN124 containing hTRT minus the 3'UTR was inserted into the EcoRI site of pEGFP-C2 such that the orientation of the hTRT is the same as the EGFP domain.

5 **pGRN139**

The oligonucleotide 5'- CTGCCCTCAGACTTCAAGACCATCCTGGACTACAAGG  
ACGACGATGACAAATGAATTCAGATCTGCGGCCGCCACCGCGGTGGAGCTC  
CAGC-3 (SEQ ID NO:150) was used to insert the IBI Flag at the C-terminus of hTRT in  
pGRN125 and create EcoRI and BglII sites for cloning. Also, COD2866 was used to  
10 convert Amp<sup>S</sup> to Amp<sup>R</sup>) and COD1941 was used to convert Cat<sup>R</sup> to Cat<sup>S</sup>.

**pGRN140**

The NcoI fragment containing the upstream sequences of genomic hTRT and the first  
intron of hTRT from lambdaG55 was inserted into the NcoI site of pBBS167. The  
fragment is oriented so that hTRT is in the same direction as the Lac promoter.

15 **pGRN141**

The NcoI fragment containing the upstream sequences of genomic hTRT and the first  
intron of hTRT from lambdaG55 was inserted into the NcoI site of pBBS167. The  
fragment is oriented so that hTRT is in the opposite direction as the Lac promoter.

**pGRN142**

20 This vector was constructed for the expression and mutagenesis of TRT sequences in *E. coli*. The promoter clone from lambda GN5 (lac orientation) was used. The selectable marker that is used with this vector is ampicillin. The NotI fragment from lambdaGphi5 containing the complete ~15 kbp genomic insert including the hTRT gene promoter region was inserted in the NotI site of plasmid pBBS185. The fragment is oriented so that the  
25 hTRT ORF is in the opposite orientation as the Lac promoter.

**pGRN143**

This vector was constructed for the expression and mutagenesis of TRT sequences in *E. coli*. The NotI fragment from lambdaGphi5 containing the complete ~15 kbp genomic insert including the hTRT gene promoter region was inserted in the NotI site of plasmid

pBBS185. The fragment is oriented so that the hTRT ORF is in the same orientation as the Lac promoter. The selectable marker that is used with this vector is ampicillin.

**pGRN144**

SAL1 deletion of pGRN140 to remove lambda sequences.

5 **pGRN145**

This vector was constructed for the expression of hTRT sequences in mammalian cells. The EcoRI fragment from pGRN137 containing the hTRT coding sequence was inserted into the EcoRI site of pBBS212 to remove the portion of the sequence corresponding to the 5'UTR of hTRT mRNA. The hTRT coding sequence is oriented so that it is expressed  
10 under the control of the MPSV promoter. The selectable markers used with this vector are Chlor/HygB/PAC.

**pGRN146**

This vector was constructed for the expression of hTRT sequences in mammalian cells. The Sse8387I-NotI fragment from pGRN130 containing the D869A mutation of hTRT was  
15 inserted into the Sse8387I-NotI sites of pGRN137. The selectable markers used with this vector are Ampicillin/HygB/PAC.

**pGRN147**

The Sse8387I-NotI fragment from pGRN139 containing the IBI Flag was inserted into the Sse8387I-NotI sites of pGRN137.

20 **pGRN148**

The BglII-Eco47III fragment from pGRN144 containing the promoter region of hTRT was inserted into the BglII-NruI sites of pSEAP2 to make an hTRT promoter/reporter construct.

**pGRN149**

25 This vector was constructed for the expression and mutagenesis of TRT sequences in *E. coli*. The mutagenic oligo 5'-cttcaagaccatcctggactttcgaaacgcggccgccaccgcggtggagctcc-3' was used to add a CSP45I site at the C-terminus of hTRT by *in vitro* mutagenesis of pGRN125. The "stop" codon of hTRT was deleted and replaced with a Csp45I site. The selectable marker that is used with this vector is ampicillin.

**pGRN150**

The BglII-FspI fragment from pGRN144 containing the promoter region of hTRT was inserted into the BglII-NruI sites of pSEAP2 to make an hTRT promoter/reporter construct.

5 **pGRN151**

This vector was constructed for the expression of hTRT sequences in mammalian cells. The EcoRI fragment from pGRN147 containing the hTRT coding sequence was inserted into the EcoRI site of pBBS212 to remove the portion of the sequence corresponding to the 5'UTR of the hTRT mRNA. The hTRT coding sequence is oriented so that it is  
10 expressed under the control of the MPSV promoter. The selectable markers used with this vector are Chlor/HygB/PAC.

**pGRN152**

The EcoRI fragment from pGRN146 containing the hTRT coding sequence was inserted into the EcoRI site of pBBS212 to remove the portion of the sequence corresponding to  
15 the 5'UTR of the hTRT. The hTRT coding sequence is oriented so that it is expressed under the control of the MPSV promoter.

**pGRN153**

The StyI fragment from pGRN130 containing the D869-->A mutation of hTRT (hTRT variant coding sequence) was inserted into the StyI sites of pGRN158 to make a plasmid  
20 containing the hTRT coding sequence with a Kozak consensus sequence at its 5'-end, an IBI FLAG sequence at its 3'-end (the C-terminus encoding region), and the D869-->A mutation.

**pGRN154**

This vector was constructed for the expression of hTRT sequences in mammalian cells.  
25 The EcoRI fragment of pGRN153 containing the hTRT gene was inserted into the EcoRI site of plasmid pBS212 in an orientation such that the hTRT ORF is oriented in the same direction as the MPSV promoter. This makes an MPSV-directed expression plasmid that expresses the hTRT protein with a Kozak consensus sequence at its amino-terminal end, an IBI FLAG at its carboxy-terminal end, and the D869-->A mutation. The selectable  
30 markers used with this vector are Ampicillin/HygB/PAC.

**pGRN155**

This vector was constructed for the expression of hTERT sequences in mammalian cells. The insert included full length cDNA of hTERT minus 5' and 3' UTR, and Kozak sequences. The EcoRI fragment from pGRN145 containing the hTERT cDNA with the Kozak  
5 consensus and no 3' or 5' UTR was inserted into the EcoRI site of p91023(B) such that the hTERT is in the same orientation as the DHFR ORF. This makes a transient expression vector for hTERT. The selectable marker used with this vector is tetracycline.

**pGRN156**

This vector was constructed for the expression of hTERT sequences in mammalian cells.  
10 The EcoRI fragment from pGRN146 containing the D869A mutation of the hTERT cDNA with the Kozak consensus and no 3' or 5' UTR was inserted into the EcoRI site of p91023(B) such that the hTERT is in the same orientation as the DHFR ORF. This makes a transient expression vector for hTERT. The insert included full length cDNA of hTERT minus 5' and 3' UTR, D869A, and Kozak sequences. The selectable marker used with this  
15 vector is tetracycline.

**pGRN157**

This vector was constructed for the expression of hTERT sequences in mammalian cells. The EcoRI fragment from pGRN147 containing the hTERT cDNA with the IBI FLAG at the C-terminus; the Kozak consensus and no 3' or 5' UTR into the EcoRI site of p91023(B)  
20 such that the hTERT is in the same orientation as the DHFR ORF. This makes a transient expression vector for hTERT. The insert included full length cDNA of hTERT minus 5' and 3' UTR, the IBI FLAG sequence, and Kozak sequences. The selectable marker used with this vector is tetracycline.

**pGRN158**

25 This vector was constructed for the expression and mutagenesis of TRT sequences in *E. coli*. The EcoRI fragment from pGRN151 containing the hTERT ORF was inserted into the EcoRI site of pBBS183 so that the hTERT ORF is oriented in the opposite direction as the Lac promoter. The insert included full length cDNA of hTERT minus 5' and 3' UTR, IBI FLAG sequence, and Kozak sequences. The hTERT coding sequence is driven by a T7  
30 promoter. The selectable marker used with this vector is ampicillin.

**pGRN159**

This vector was constructed for the expression and mutagenesis of TRT sequences in *E. coli*. The NheI-KpnI fragment from pGRN138 containing the EGFP to hTRT fusion was inserted into the XbaI-KpnI sites of pBluescriptIIKS+. This makes a T7 expression vector  
5 for the fusion protein (the coding sequence is driven by a T7 promoter). The insert included full length cDNA of hTRT minus the 3' UTR as a fusion protein with EGFP. The selectable marker used with this vector is ampicillin.

**pGRN160**

This vector was constructed for the expression of *antisense* hTR sequences in mammalian  
10 cells. The coding sequence is operably linked to an MPSV promoter. The XhoI-NsiI fragment from pGRN90 containing the full length hTR ORF was inserted into the Sall-Sse8387I sites of pBBS295. This makes a transient/stable vector expressing hTR antisense RNA. A GPT marker was incorporated into the vector. The selectable markers used with this vector are Chlor/gpt/PAC.

**pGRN161**

This vector was constructed for the expression of *sense* hTR sequences in mammalian cells. The XhoI-NsiI fragment from pGRN89 containing the full length hTR ORF was inserted into the Sall-Sse8387I sites of pBBS295. This makes a transient/stable vector expressing hTR in the sense orientation. The coding sequence is driven by an MPSV  
20 promoter. A GPT marker was incorporated into the vector. The selectable markers used with this vector are Chlor/gpt/PAC.

**pGRN162**

The XhoI-NsiI fragment from pGRN87 containing the full length hTR ORF was inserted into the Sall-Sse8387I sites of pBBS295. This makes a transient/stable vector expressing  
25 truncated hTR (from position +108 to +435) in the sense orientation.

**pGRN163**

This vector was constructed for the expression and mutagenesis of TRT sequences in *E. coli*. The coding sequence is driven by a T7 promoter. Oligonucleotide RA45 (5'-GCCACCCCCGCGCTGCCTCGAGCTCCCCGCTGC-3') (SEQ ID NO:151) is used  
30 is used in *in vitro* mutagenesis to change the initiating met in hTRT to Leu and introduce

an XhoI site in the next two codons after the Leu. Also COD 1941 was used to change CatR to CatS, and introduces a BSPH1 site, and COD 2866 was used to change AmpS to AmpR, introducing an FSP1 site. The selectable marker used with this vector is ampicillin.

5     **pGRN164**

This vector was constructed for the expression of hTR sequences in *E. coli*. Primers hTR+1 5'-GGGGAAGCTTTAATACGACTCACTATAGGGTTGCGGAGGGTGG GCCTG-3' and hTR+45 5'-CCCCGGATCCTGCGCATGTGTGAGCCGAGTCCT GGG-3' (SEQ ID NO:152) were used to amplify by PCR a fragment from pGRN33  
10     containing the full length hTR with the T7 promoter on the 5' end (as in hTR+1). A BamHI-HindIII digest of the PCR product was put into the BamHI-HindIII sites of pUC119. The coding sequence operably linked to a T7 promoter. The selectable marker used with this vector is ampicillin.

**pGRN165**

15     This vector was constructed for the expression and mutagenesis of hTRT sequences in *E. coli*. The coding sequence is operably linked to a T7 promoter. The EcoRI fragment from pGRN145 containing the hTRT ORF with a Kozak front end was inserted into the EcoRI site of pBluescriptIIISK+ so that the hTRT is oriented in the same direction as the T7 promoter. The selectable marker used with this vector is ampicillin.

20     **pGRN166**

This vector was constructed for the expression and mutagenesis of TRT sequences in mammalian cells. The coding sequence is operably linked to a T7 promoter. The EcoRI fragment from pGRN151 containing the hTRT ORF with a Kozak front end and IBI flag at the back end was inserted into the EcoRI site of pBluescriptIIISK+ so that the hTRT ORF  
25     is oriented in the same direction as the T7 promoter. The insert included full length cDNA of hTRT minus 5' and 3' UTR, FLAG sequence (Immuncx Corp, Seattle WA), and Kozak sequences. The selectable marker used with this vector is ampicillin.

**pGRN167**

30     AvrII-StuI fragment from pGRN144 containing the 5' end of the hTRT ORF was inserted into the XbaI-StuI sites of pBBS161.

**pGRN168**

This vector was constructed for the expression of hTERT sequences in mammalian cells. The EcoRI fragment from pGRN145 containing the optimized hTERT expression cassette was inserted into the EcoRI site of pIND such that the hTERT coding sequence is in the same orientation as the miniCMV promoter. The selectable markers used with this vector are ampicillin/neomycin/kanamycin.

**pGRN169**

This vector was constructed for the expression of *antisense* hTERT sequences in mammalian cells. The EcoRI fragment from pGRN145 containing the optimized hTERT expression cassette was inserted into the EcoRI site of pIND such that the hTERT is in the reverse orientation from the miniCMV promoter. The hTERT was cloned into the Ecdysone-Inducible Expression System from Invitrogen. The insert included full length cDNA of hTERT minus 5' and 3' UTR, and Kozak sequences. The selectable markers used with this vector are ampicillin/neomycin/kanamycin.

**pGRN170**

This vector was constructed for the expression of *antisense* hTERT sequences in mammalian cells. The EcoRI fragment from pGRN145 containing the optimized hTERT expression cassette was inserted into the EcoRI site of pIND(sp1) such that the hTERT is in the opposite orientation from the miniCMV promoter. The hTERT was cloned into the Ecdysone-Inducible Expression System from Invitrogen, with a pIND(sp1) sequence. The insert included full length cDNA of hTERT minus 5' and 3' UTR, and Kozak sequences. The selectable markers used with this vector are ampicillin/neomycin/kanamycin.

**pGRN171**

The Eco47III-NarI fragment from pGRN163 was inserted into the Eco47III-NarI sites of pGRN167, putting the M1L mutation into a fragment of the hTERT genomic DNA.

**pGRN172**

The BamHI-StuI fragment from pGRN171 containing the Met to Leu mutation in the hTERT ORF was inserted into the BglII-NruI sites of pSEAP2-Basic.

**pGRN173**

This vector was constructed to analyze the transcriptional activity of TRT sequences; specifically, this is an intron construct to determine whether the first hTRT intron has promoter activity. The EcoRV-ECO47III fragment from pGRN144 containing the 5' end  
5 of the hTRT promoter region was inserted into the SrfI-Eco47III sites of pGRN172. This makes a promoter reporter plasmid that contains the promoter region of hTRT from approximately 2.3 kb upstream from the start of the hTRT ORF to just after the first intron in the coding region, with the Met1-->Leu mutation. The selectable marker used with this vector is ampicillin.

**10 pGRN174**

This vector was constructed for the expression of hTRT sequences in mammalian cells, and is an inducible hTRT expression vector. The EcoRI fragment from pGRN145 containing the "optimized" hTRT expression cassette was inserted into the EcoRI site of pIND(sp1) such that the hTRT is in the same orientation as the miniCMVpromoter. This  
15 makes a promoter reporter plasmid that contains the promoter region of the hTRT gene from approximately 2.3 kb upstream from the start of the hTRT ORF to just after the first intron in the coding region. The insert included full length cDNA of hTRT minus 5' and 3' UTR, and Kozak sequences. The selectable markers used with this vector are ampicillin/neomycin/kanamycin.

20

From the above, it is clear that the present invention provides nucleic acid and amino acid sequences, as well as other information regarding telomerase, telomerase protein subunits, and motifs from various organisms, in addition to methods for identification of homologous structures in other organisms in addition to those described  
25 herein.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing  
30 from the scope and spirit of the invention. Although the invention has been described in



connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of

5 the following claims.

**We claim:**

1. An isolated, substantially pure, or recombinant protein preparation of a TRT protein, or a variant thereof, or a fragment thereof.
- 5 2. An isolated, substantially pure, or recombinant TRT protein, said protein characterized by having an amino acid sequence with at least 75% sequence identity to the TRT protein that has a sequence set forth in SEQ ID NOS:2, 4-6, 52, 58, 61, 63, 64, 65, 67, or 68, or a variant thereof, or a fragment thereof.
- 10 3. An isolated TRT protein, or a variant thereof, or a fragment thereof, said protein:
  - (i) having a calculated molecular weight of about 50 to 150 kDa; and
  - (ii) (a) specifically binding to an antibody raised against a protein, or immunogenic fragment thereof, that has a sequence set forth in SEQ ID NO:2, 4-6, 52, 58, 61, 63, 64, 65, 67, or 68; or
  - 15 (c) having 60% amino acid sequence identity to a protein that has a sequence set forth in SEQ ID NO:2, 4-6, 52, 58, 61, 63, 64, 65, 67, or 68.
4. The protein of claims 1 to 3 that has the sequence set forth in SEQ ID NOS:2, 4-6, 52, 58, 61, 63, 64, 65, 67 or 68, or a variant thereof or a fragment thereof.
- 20 5. The TRT protein of claims 1 to 3 wherein the TRT protein is produced by recombinant means or synthetic means.
6. The TRT protein of claims 1 to 3 wherein the TRT protein is encoded by a nucleic acid molecule which specifically hybridizes to SEQ ID NOS:1, 3, 19, 53, 62, 66 or 69.
- 25 7. The TRT protein of claims 1 to 3 wherein the protein, variant, or fragment has telomerase catalytic activity.

8. The TRT protein of claims 1 to 3 wherein the protein, variant, or fragment does not have telomerase catalytic activity.
9. The TRT protein fragment of claims 1 to 3 that comprises at least 6 amino acid  
5 residues.
10. An isolated, synthetic, substantially pure, or recombinant polynucleotide comprising a nucleic acid sequence that encodes a TRT protein or variant thereof or a fragment thereof.
- 10
11. An isolated, synthetic, substantially pure, or recombinant polynucleotide selected from:
- (a) the DNA having a sequence as set forth in SEQ ID NOS:2, 4-6, 52, 58, 61, 63, 64, 65, 67 or 68;
- 15 (b) a polynucleotide of at least 10 nucleotides which hybridizes to the foregoing DNA and which codes for a TRT protein or variant;
- (c) the DNA having a sequence that encodes a polypeptide encoded by a polynucleotide of (a) or (b).
- 20 12. An isolated nucleic acid encoding a TRT protein, said protein defined as follows:
- (i) having a calculated molecular weight of between 50 and 150 kDa; and
- (ii) (a) specifically binding to an antibody raised against a TRT protein, or a immunogenic fragment thereof; or
- (b) having at least 60% amino acid sequence identity to a TRT protein.
- 25
13. The isolated nucleic acid of claims 10 to 12, wherein the TRT protein is from *Euplotes*, *Schizosaccharomyces*, *Tetrahymena*, *Oxytrichia*, mouse, or mammals.
14. The isolated nucleic acid of claims 10 to 12, wherein the calculated molecular  
30 weight of the encoded telomerase reverse transcriptase protein is about 123 to 127 kDa.

15. The isolated nucleic acid of claims 10 to 12, wherein the encoded TRT protein has at least 80% amino acid sequence identity to a TRT protein comprising SEQ ID NOS:2, 4-6, 52, 58, 61, 63, 64, 65, 67 or 68.
- 5 16. An isolated nucleic acid which specifically hybridizes to SEQ ID NOS:1, 3, 19, 53, 62, 66, or 69 under stringent conditions.
17. An isolated nucleic acid encoding a protein that specifically binds to an antibody directed against the protein, or immunogenic fragment thereof, and that has a sequence set  
10 forth in SEQ ID NO:2, 4-6, 52, 58, 61, 63, 64, 65, 67 or 68.
18. An isolated nucleic acid that has a nucleotide sequence encoding at least about five contiguous amino acids of a TRT having an amino acid sequence as set forth in SEQ ID NO:2, 4-6, 52, 58, 61, 63, 64, 65, 67 or 68, or variants thereof.
- 15 19. An expression vector that has the nucleic acid sequence any of the claims 10 to 18.
20. A cell comprising a polynucleotide as defined in any of the claims 10 to 19.
- 20 21. A transfected cell that has a heterologous gene coding for at least 10 nucleotides of a TRT protein-encoding nucleic acid.
22. A transfected cell into which has been introduced an exogenous nucleic acid sequence which specifically hybridizes under stringent conditions to the nucleic acid of  
25 claims 10 to 18, has been introduced, and which expresses the exogenous nucleic acid as a TRT protein.
23. The transfected cell of claim 21 or 22, wherein the transfected cell is a mortal, karyotypically normal, diploid cell.

30

24. The transfected cell of claim 21 or 22, wherein said cell is derived from a bacterium, an insect, a plant, a fungus, a yeast or a mammal.
25. The transfected cell of claim 21 or 22 that is contained within a non-human animal  
5 or progeny thereof.
26. A non-human animal, or progeny thereof, into which an exogenous nucleic acid sequence which specifically hybridizes under stringent conditions to the nucleic acid of claims 10 to 19, has been introduced and the animal expresses the exogenous nucleic acid  
10 as a TRT protein.
27. A transgenic non-human animal that has a heterologous gene coding for at least 10 nucleotides of a TRT protein-encoding nucleic acid.
- 15 28. The non-human animal of claim 26 or 27, wherein the animal is a mouse.
29. The non-human animal of claim 26 or 27, wherein said animal comprises a recombinant TRT gene that differs from a naturally occurring TRT gene in one or more codons.  
20
30. The non-human animal of claim 29, wherein said gene differs from a naturally occurring TRT gene by having a substitution, missense mutation, a nonsense mutation, an insertion, or a deletion.
- 25 31. The non-human animal of claim 26 or 27, wherein said animal is deficient in a telomerase activity.

32. The non-human animal of claim 31, wherein said deficiency is a result of a gene encoding a telomerase having a reduced level of a telomerase activity compared to a wild-type telomerase.
- 5 33. An antibody, or binding fragment thereof, wherein the antibody or fragment specifically binds to a TRT protein or immunogenic fragment thereof.
34. An antibody, specifically immunoreactive under immunologically reactive conditions, to a TRT protein, or immunogenic fragment thereof, said protein having an  
10 amino acid sequence as set forth in SEQ ID NO:2, 4-6, 52, 58, 61, 63, 64, 65, 67, or 68.
35. An antibody, specifically immunoreactive under immunologically reactive conditions, to a TRT protein, or immunogenic fragment thereof, comprising the protein  
15 encoded by the nucleic acid of claims 10 to 18.
36. The use of a polynucleotide that is at least ten nucleotides to 10 kb in length and comprises a contiguous sequence of at least ten nucleotides that is identical or exactly complementary to a contiguous sequence in a naturally occurring TRT gene or TRT  
20 mRNA in assaying or screening for a TRT gene sequence or TRT mRNA.
37. The use of a polynucleotide that is at least ten nucleotides to 10 kb in length and comprises a contiguous sequence of at least ten nucleotides that is identical or exactly complementary to a contiguous sequence in a naturally occurring TRT gene or TRT  
25 mRNA in preparing a recombinant host cell.
38. A method of determining whether a compound or treatment is a modulator of a TRT activity or expression comprising detecting a change in activity or expression in a cell, animal or composition comprising a TRT recombinant protein or polynucleotide  
30 following administration of the compound or treatment.

39. A method of determining whether a test compound is a modulator of a TRT activity, said method comprising the steps of;

(a) contacting a TRT protein of claims 1 to 9 with the test compound; and

5 (b) measuring the activity of the TRT protein, wherein a change in the TRT activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the telomerase reverse transcriptase activity.

40. A method of preparing recombinant telomerase, said method comprising contacting  
10 a recombinant TRT protein of claims 1 to 9 with a telomerase RNA component under conditions such that said recombinant protein and said telomerase RNA component associate to form a telomerase enzyme capable of catalyzing the addition of nucleotides to a telomerase substrate.

15 41. A method of detecting a TRT gene product in a sample comprising:

(a) contacting the sample with a probe that specifically binds the gene product, wherein the probe and the gene product form a complex, and detecting the complex; or

(b) specifically amplifying the gene product in the biological sample, wherein said gene product is a nucleic acid, and detecting the amplification product;

20 wherein the presence of the complex or amplification product is correlated with the presence of the TRT gene product in the biological sample.

42. A method of detecting the presence of at least one telomerase positive human cell in a biological sample comprising human cells, said method comprising the steps:

25 (a) measuring the amount of a TRT gene product in said sample,

(b) comparing the amount measured with a control correlating to a sample lacking telomerase positive cells,

wherein the presence of a higher level of the TRT gene product in said sample as compared to said control is correlated with the presence of telomerase positive cells in the  
30 biological sample.

43. A method for diagnosing a telomerase-related condition in a mammal, comprising:
- (a) obtaining a cell or tissue sample from the mammal;
  - (b) determining the amount of a TRT gene product in the cell or tissue; and
  - (c) comparing the amount of TRT gene product in the cell or tissue with the
- 5 amount in a healthy cell or tissue of the same type;
- wherein a different amount of TRT gene product in the sample from the mammal and the healthy cell or tissue is diagnostic of a telomerase-related condition.
44. A method for increasing the proliferative capacity of a vertebrate cell *in vitro* by
- 10 increasing expression of TRT in the cell.
45. The use of an agent which increases the expression or activity of a TRT in the manufacture of a medicament for the treatment of a condition addressed by increasing proliferative capacity of a vertebrate cell.
- 15
46. The use defined in claim 45 wherein the medicament is for inhibiting an effect of ageing.
47. A pharmaceutical composition comprising an acceptable carrier and a TRT protein,
- 20 variant or fragment of claims 1 to 9, a TRT antibody or binding fragment of claims 33 to 35, a polynucleotide encoding a TRT protein, variant or fragment as defined in claims 10 to 18, or a nucleic acid that encodes a TRT protein or subsequence thereof.
48. The use of an inhibitor of telomerase expression or activity in the manufacture of
- 25 a medicament for the treatment of a condition associated with an elevated level of telomerase activity within a mammalian cell, said inhibitor being a polynucleotide of claims 10 to 9 or a polypeptide of claims 1 to 8 or a compound discovered using any of the foregoing.



49. A protein, variant or fragment of any one of claims 1 to 9 for use as a pharmaceutical.
50. The use of a protein, variant or fragment of any one of claims 1 to 9 in the  
5 manufacture of a medicament.
51. The use of a protein, variant or fragment of any one of claims 1 to 9 in the manufacture of a medicament for inhibiting an effect of ageing or cancer.
- 10 52. A polynucleotide or fragment of claims 10 to 18 for use as a pharmaceutical.
53. The use of a polynucleotide or fragment of claims 10 to 18 in the manufacture of a medicament.
- 15 54. The use of a polynucleotide or fragment of claims 10 to 18 in the manufacture of a medicament for for inhibiting an effect of ageing or cancer.
55. The use of claims 51 and 54 wherein the medicament's inhibitory effect on ageing increases the lifespan of a cell or an animal to which the medicament is administered.
- 20 56. A method for detecting the presence of a polynucleotide sequence encoding at least a portion of a TRT in a biological sample, comprising the steps of:
- a) providing:
    - 25 i) a biological sample suspected of containing a nucleic acid corresponding to the polynucleotide sequence of a TRT;
    - ii) a probe comprising a nucleotide sequence of a TRT, or a fragment thereof capable of hybridizing to a telomerase reverse transcriptase from a biological sample;

- b) combining said nucleic acid-containing biological sample with said probe under conditions such that a hybridization complex is formed between said nucleic acid and said probe; and
- c) detecting said hybridization complex.

5

57. The method of claim 56, wherein, said nucleic acid in said biological sample is ribonucleic acid.

58. The method of claim 56, wherein said detected hybridization complex correlates  
10 with expression of a TRT in said biological sample.

59. The method of claim 56, wherein, said nucleic acid in said biological sample is deoxyribonucleic acid.

15 60. The method of Claim 56, wherein said detecting of said hybridization complex comprises the detection of alterations in the nucleotide sequence of a TRT in said biological sample.

61. The use of a polynucleotide or fragment comprising a purified antisense nucleotide  
20 having a nucleic acid sequence complementary to at least a portion of the TRT polynucleotide of claim 10 to 18 in the manufacture of a medicament.

62. The use of claim 61, wherein the polynucleotide or fragment has a nucleic acid sequence complementary to the nucleic acid sequence set forth in SEQ ID NO: 1, 3, 19,  
25 53, 62, 66 or 69.

63. The use of claim 61 wherein the polynucleotide is inserted in a recombinant expression vector.

64. A method for producing a polypeptide comprising an amino acid sequence encoded by a nucleotide sequence of claim 10 to 18, the method comprising culturing a host cell comprising a nucleotide sequence of claims 10 to 18 under conditions suitable for the expression of the polypeptide encoded therein.

5

65. The method of claim 64, further comprising a step wherein the polypeptide is isolated or purified.

66. A method for detecting the expression or presence of a TRT in a biological sample comprising the steps of:

10

a) providing:

- i) a biological sample suspected of expressing TRT protein; and
- ii) the antibody of Claims 33 to 35;

b) combining said biological sample and said antibody under conditions such that an antibody:TRT protein complex is formed; and

15

c) detecting said complex wherein the presence of said complex correlates with the expression or presence of said TRT in said biological sample.

67. A substantially purified polypeptide comprising at least a portion of the amino acid sequence selected from the group consisting of SEQ ID NO:4-6, or variants thereof, or fragments thereof.

20

68. The polypeptide of Claim 67, wherein said portion of said polypeptide comprises fragments of SEQ ID NO:4-6, having a length greater than 6 amino acids.

25

69. The polypeptide sequence of Claim 67, wherein said variant is a homologue derived from human cells.

70. An isolated polynucleotide sequence encoding the polypeptide of Claim 67, or variants thereof, or fragments thereof.

30

71. The polynucleotide sequence of Claim 70, comprising at least a portion of the nucleic acid sequence of SEQ ID NO:3, or variants thereof, or fragments thereof.

72. The polynucleotide sequence of Claim 70, wherein said portion of said  
5 polynucleotide comprises fragments of SEQ ID NO:3 having a length greater than 10 nucleotides.

73. The polynucleotide sequence of Claim 70, wherein said variants is a homologue  
10 derived from human cells.

74. A telomerase complex comprised of i) a purified TRT protein subunit, or variants thereof; ii) a purified 43 kDa telomerase protein subunit or homologue thereof, or variants thereof, and iii) a purified telomerase RNA.

75. The telomerase complex of Claim 74, wherein said TRT protein subunit is obtained  
15 from *Euplotes aediculatus*.

76. The telomerase complex of Claim 74, wherein said TRT protein subunit is encoded  
20 by SEQ ID NO:1.

77. The telomerase complex of Claim 74, wherein said telomerase complex is capable  
of full or partial telomerase activity.

78. The telomerase complex of Claim 74, wherein said telomerase complex is capable  
25 of replicating telomeric DNA.

79. The telomerase complex of claim 74, wherein said 43 kDa telomerase protein subunit  
homologue or variant is derived from human cells.

80. A composition comprising a TRT protein of claims 1 to 8 and an RNA.  
30

81. The composition of claim 80, wherein said RNA is a telomerase RNA (TR).
82. The composition of claim 80, wherein the TRT protein and the TR form a ribonucleoprotein complex with a full or partial telomerase activity.
- 5 83. Substantially pure telomerase comprising TRT and TR.
84. The telomerase of claim 83 that is at least about 95% pure.
- 10 85. The telomerase of claim 83 that has been isolated from a cell.
86. An isolated TRT polypeptide comprising an amino acid sequence comprising a motif of contiguous amino acids selected from the group consisting of: a) AA<sub>1</sub>-AA<sub>2</sub>-AA<sub>3</sub>-AA<sub>4</sub>-AA<sub>5</sub>-AA<sub>6</sub>-AA<sub>7</sub>-AA<sub>8</sub>-AA<sub>9</sub>-AA<sub>10</sub>-AA<sub>11</sub>-AA<sub>12</sub>-AA<sub>13</sub>; b) AA<sub>14</sub>-AA<sub>15</sub>-AA<sub>16</sub>-AA<sub>17</sub>-AA<sub>18</sub>-AA<sub>19</sub>-AA<sub>20</sub>-AA<sub>21</sub>-AA<sub>22</sub>-AA<sub>23</sub>-AA<sub>24</sub>-AA<sub>25</sub>-AA<sub>26</sub>; c) AA<sub>27</sub>-AA<sub>28</sub>-AA<sub>29</sub>-AA<sub>30</sub>-AA<sub>31</sub>-AA<sub>32</sub>-AA<sub>33</sub>-AA<sub>34</sub>-AA<sub>35</sub>-AA<sub>36</sub>; d) AA<sub>37</sub>-AA<sub>38</sub>-AA<sub>39</sub>-AA<sub>40</sub>-AA<sub>41</sub>-AA<sub>42</sub>-AA<sub>43</sub>-AA<sub>44</sub>; and, e) AA<sub>45</sub>-AA<sub>46</sub>-AA<sub>47</sub>-AA<sub>48</sub>-AA<sub>49</sub>-AA<sub>50</sub>-AA<sub>51</sub>-AA<sub>52</sub>,  
 wherein, AA<sub>1</sub> is a hydrophobic amino acid or cysteine; AA<sub>2</sub> is any amino acid; AA<sub>3</sub> is any amino acid; AA<sub>4</sub> is a hydrophobic amino acid or aspartic acid; AA<sub>5</sub> is aspartic acid;  
 20 AA<sub>6</sub> is a hydrophobic amino acid or tyrosine; AA<sub>7</sub> is any amino acid; AA<sub>8</sub> is any amino acid; AA<sub>9</sub> is any amino acid; AA<sub>10</sub> is a hydrophobic amino acid or tyrosine; AA<sub>11</sub> is any amino acid; AA<sub>12</sub> is any amino acid; AA<sub>13</sub> is a hydrophobic amino acid; AA<sub>14</sub> is a hydrophobic amino acid, glutamine, arginine, or glycine; AA<sub>15</sub> is any amino acid; AA<sub>16</sub> is any amino acid; AA<sub>17</sub> is any amino acid; AA<sub>18</sub> is any amino acid; AA<sub>19</sub> is any amino acid; AA<sub>20</sub> is glutamine; AA<sub>21</sub> is glycine; AA<sub>22</sub> is any amino acid; AA<sub>23</sub> is any amino acid; AA<sub>24</sub> is any amino acid; AA<sub>25</sub> is serine; AA<sub>26</sub> is any amino acid; AA<sub>27</sub> is a hydrophobic amino acid, histidine or tyrosine; AA<sub>28</sub> is any amino acid; AA<sub>29</sub> is any amino acid; AA<sub>30</sub> is any amino acid; AA<sub>31</sub> is a hydrophobic amino acid or threonine; AA<sub>32</sub> is aspartic acid; AA<sub>33</sub> is aspartic acid; AA<sub>34</sub> is a hydrophobic amino acid or tyrosine; AA<sub>35</sub> is a hydrophobic amino acid, tyrosine or lysine; AA<sub>36</sub> is a hydrophobic amino acid; AA<sub>37</sub>
- 25
- 30

is glycine; AA<sub>38</sub> is a hydrophobic amino acid or cysteine; AA<sub>39</sub> is any amino acid; AA<sub>40</sub> is a hydrophobic amino acid, lysine, or threonine; AA<sub>41</sub> is any amino acid; AA<sub>42</sub> is any amino acid; AA<sub>43</sub> is any amino acid; AA<sub>44</sub> is lysine; AA<sub>45</sub> is a hydrophobic amino acid, cysteine, lysine, or tyrosine; AA<sub>46</sub> is any amino acid; AA<sub>47</sub> is a hydrophobic amino acid, tryptophan, serine, or tyrosine; AA<sub>48</sub> is any amino acid; AA<sub>49</sub> is glycine; AA<sub>50</sub> is a hydrophobic amino acid or tyrosine; AA<sub>51</sub> is any amino acid; and, AA<sub>52</sub> is a hydrophobic amino acid or arginine or glutamine.

87. The TRT polypeptide of Claim 86, comprising an amino acid sequence comprising a motif of contiguous amino acids consisting of

AA<sub>1</sub>-AA<sub>2</sub>-AA<sub>3</sub>-AA<sub>4</sub>-AA<sub>5</sub>-AA<sub>6</sub>-AA<sub>7</sub>-AA<sub>8</sub>-AA<sub>9</sub>-AA<sub>10</sub>-AA<sub>11</sub>-AA<sub>12</sub>-AA<sub>13</sub>.

88. The TRT polypeptide of Claim 87, wherein: AA<sub>1</sub> is a hydrophobic amino acid or cysteine; AA<sub>2</sub> is any amino acid; AA<sub>3</sub> is threonine, lysine, tyrosine or glutamic acid; AA<sub>4</sub> is a hydrophobic amino acid or aspartic acid; AA<sub>5</sub> is aspartic acid; AA<sub>6</sub> is a hydrophobic amino acid or tyrosine; AA<sub>7</sub> is glutamic acid, lysine or glycine; AA<sub>8</sub> is any amino acid; AA<sub>9</sub> is cysteine or alanine; AA<sub>10</sub> is a hydrophobic amino acid, tyrosine or phenylalanine; AA<sub>11</sub> is aspartic acid or phenylalanine; AA<sub>12</sub> is serine or threonine; and, AA<sub>13</sub> is a hydrophobic amino acid.

20

89. The TRT polypeptide of Claim 88, wherein: AA<sub>1</sub> is phenylalanine; AA<sub>2</sub> is any amino acid; AA<sub>3</sub> is threonine or lysine; AA<sub>4</sub> is methionine, phenylalanine, valine; AA<sub>5</sub> is aspartic acid; AA<sub>6</sub> is isoleucine or valine; AA<sub>7</sub> is glutamic acid or lysine; AA<sub>8</sub> is any amino acid; AA<sub>9</sub> is cysteine or alanine; AA<sub>10</sub> is tyrosine; AA<sub>11</sub> is aspartic acid; AA<sub>12</sub> is serine or threonine; and, AA<sub>13</sub> is isoleucine or valine.

25

90. The TRT polypeptide of claims 86 to 89 wherein the polypeptide is produced by recombinant means.

91. An isolated nucleic acid encoding the polypeptide of claims 86 to 89 or variants thereof.

92. An isolated, substantially pure, or recombinant TRT polypeptide, said polypeptide  
5 characterized by having an amino acid sequence comprising:

Trp-R<sub>1</sub>-X<sub>7</sub>-R<sub>1</sub>-R<sub>1</sub>-R<sub>2</sub>-X-Phe-Phe-Tyr-X-Thr-Glu-X<sub>8,9</sub>-R<sub>3</sub>-R<sub>3</sub>-Arg-R<sub>4</sub>-X<sub>2</sub>-Trp

where X is any amino acid and a subscript refers to the number of consecutive residues, R<sub>1</sub> is leucine or isoleucine, R<sub>2</sub> is glutamine or arginine, R<sub>3</sub> is phenylalanine or tyrosine, and R<sub>4</sub> is lysine or histidine.

10

93. An isolated, substantially pure or recombinant nucleic acid that encodes a TRT polypeptide, said polypeptide characterized by having an amino acid sequence comprising:

Trp-R<sub>1</sub>-X<sub>7</sub>-R<sub>1</sub>-R<sub>1</sub>-R<sub>2</sub>-X-Phe-Phe-Tyr-X-Thr-Glu-X<sub>8,9</sub>-R<sub>3</sub>-R<sub>3</sub>-Arg-R<sub>4</sub>-X<sub>2</sub>-Trp

where X is any amino acid and a subscript refers to the number of  
15 consecutive residues, R<sub>1</sub> is leucine or isoleucine, R<sub>2</sub> is glutamine or arginine, R<sub>3</sub> is phenylalanine or tyrosine, and R<sub>4</sub> is lysine or histidine.

94. An isolated TRT polypeptide comprising an amino acid sequence comprising a motif of contiguous amino acids selected from the group consisting of: Motif T of Figure  
20 55, Motif 1 of Figure 55, Motif 2 of Figure 55, Motif A of Figure 55, Motif B' of Figure 55, Motif C of Figure 55, Motif D of Figure 55 and Motif E of Figure 55.

95. An isolated TRT polypeptide comprising an amino acid sequence comprising a motif of contiguous amino acids selected from the group consisting of: Motif T, comprising the sequence W-X<sub>12</sub>-FFY-X-TE-X<sub>10,11</sub>-R-X<sub>3</sub>-W-X<sub>7</sub>-I; Motif T' comprising the sequence E-X<sub>2</sub>-V-X; Motif 1, comprising the sequence X<sub>3</sub>R-X<sub>2</sub>PK-X<sub>3</sub>; Motif 2, comprising the sequence X-R-X-I-X; Motif A, comprising the sequence X<sub>4</sub>-F-X<sub>3</sub>-D-X<sub>4</sub>-YD-X<sub>2</sub>; Motif B', comprising the sequence Y-X<sub>4</sub>-G-X<sub>2</sub>-QG-X<sub>3</sub>-S-X<sub>8</sub>; and, Motif C, comprising the sequence X<sub>6</sub>-DD-X-L-X<sub>3</sub>;

wherein X is any amino acid, X<sub>2</sub> is any two amino acids, X<sub>3</sub> is any three amino acids, and the like.

96. An isolated TRT polypeptide comprising an amino acid sequence motif comprising  
5 the sequence  
W(L/I)XXXXhXhXh(Q/R)XFFYXTEXXXXXXXXXXXX(F/Y)(F/Y)RXXXWXX(L/I)X  
XhXIXXXX(K/M), wherein X is any amino acid and wherein h is a hydrophobic amino acid.
- 10 97. An isolated TRT polypeptide comprising an amino acid sequence motif comprising  
the sequence FFYXTE, wherein X is any amino acid.
98. An isolated TRT polypeptide comprising an amino acid sequence motif comprising  
the sequence hRhIPKK, wherein h is a hydrophobic amino acid.
- 15 99. An isolated TRT polypeptide comprising an amino acid sequence motif comprising  
the sequence hXXXXhRhIPKK, wherein h is a hydrophobic amino acid and wherein X is  
any amino acid.
- 20 100. An isolated TRT polypeptide comprising an amino acid sequence motif comprising  
the sequence P(K/E)(K/L)(Y/F)FhXhDh, wherein h is a hydrophobic amino acid and  
wherein X is any amino acid.
- 25 101. An isolated TRT polypeptide comprising an amino acid sequence motif comprising  
the sequence KXYXQXXGIPQGSXLSXhLXXhXYXDL, wherein h is a hydrophobic  
amino acid and wherein X is any amino acid.
- 30 102. An isolated TRT polypeptide comprising an amino acid sequence motif comprising  
the sequence (L/I)L(R/K)(L/V)XDD(F/Y)Lh(I/V)(T/S), wherein h is a hydrophobic amino  
acid and wherein X is any amino acid.



103. An isolated TRT polypeptide comprising an amino acid sequence motif comprising the sequence (NH<sub>2</sub>)-X<sub>300-600</sub>-W-X<sub>12</sub>-FFY-X-TE-X<sub>10-11</sub>-R-X<sub>3</sub>-W-X<sub>7</sub>-I-X<sub>5-20</sub>-E-X<sub>2</sub>-V-X-X<sub>5-20</sub>-X<sub>3</sub>-R-X<sub>2</sub>-PK-X<sub>4-10</sub>-R-X-I-X-X<sub>60-80</sub>-X<sub>4</sub>-F-X<sub>3</sub>-D-X<sub>4</sub>-YD-X<sub>2</sub>-X<sub>80-130</sub>-Y-X<sub>4</sub>-G-X<sub>2</sub>-QG-X<sub>3</sub>-S-X<sub>4</sub>-X<sub>5-35</sub>-X<sub>6</sub>-DD-X-L-X<sub>3</sub>-X<sub>10-20</sub>-X<sub>12</sub>-K, wherein h is a hydrophobic amino acid and wherein X
- 5 is any amino acid.
104. The polypeptide of claims 92 to 103 comprising an amino acid sequence of a naturally occurring TRT protein.
- 10 105. The TRT protein of claim 104 selected from the group of organisms consisting of *Euplotes*, *Tetrahymena*, *Schizosaccharomyces*, *Oxytricha*, mouse and mammals.



FIGURE 2

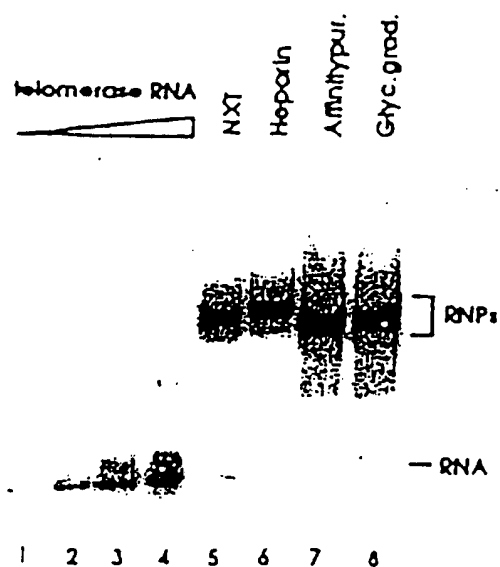


FIGURE 3

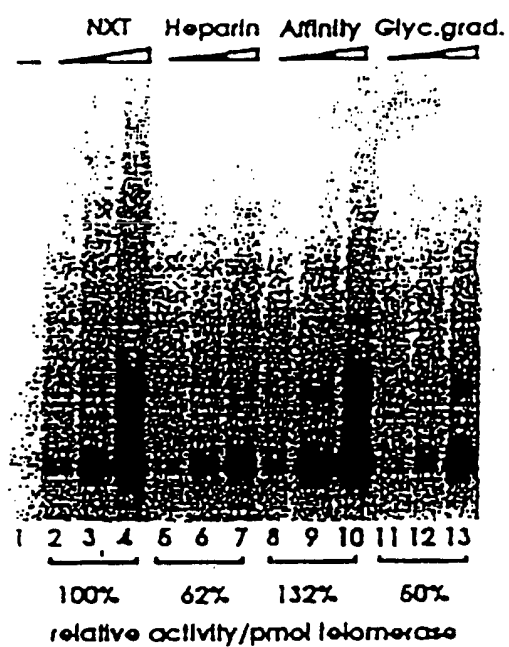


FIGURE 4

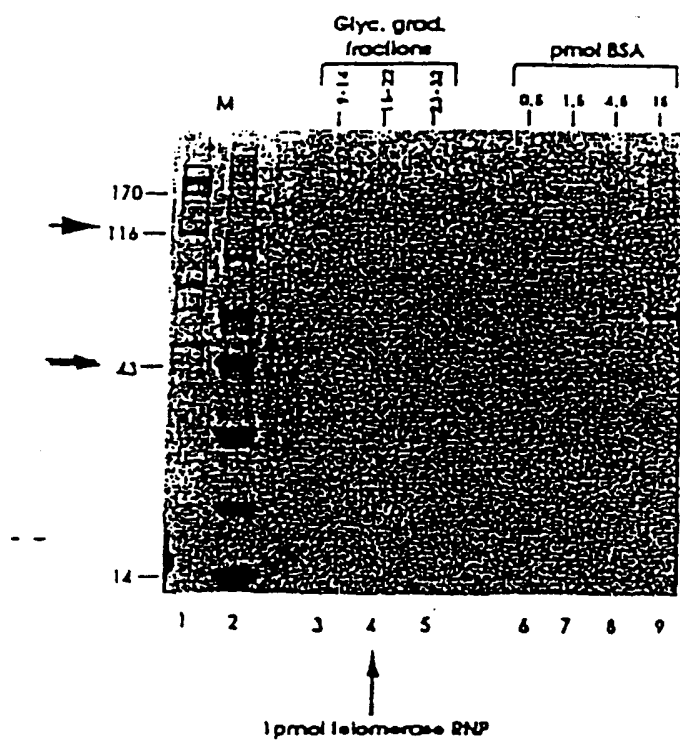


FIGURE 5

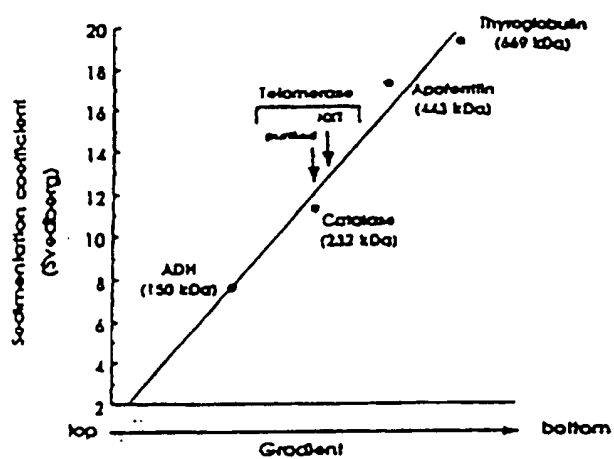


FIGURE 6

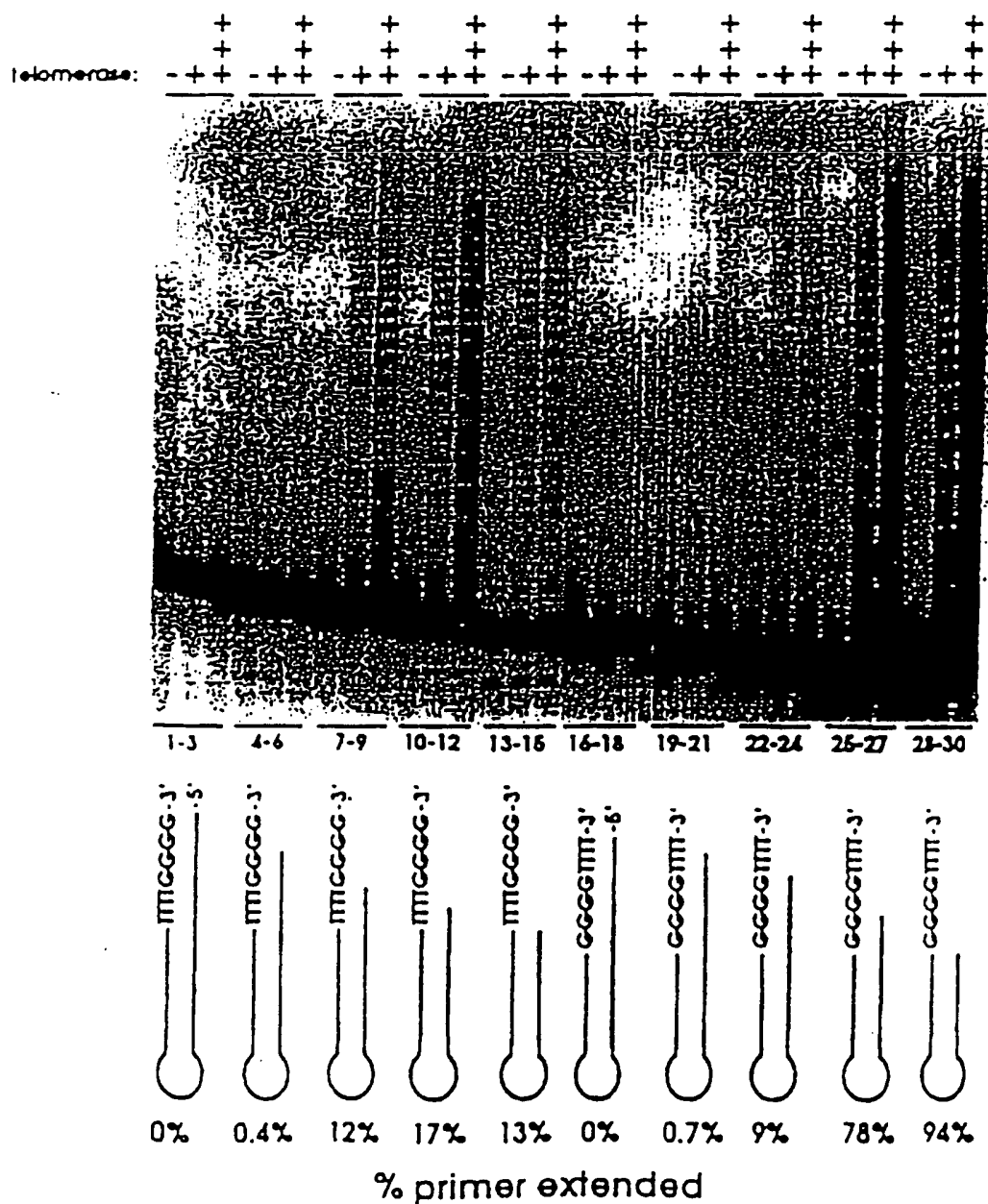


FIGURE 7

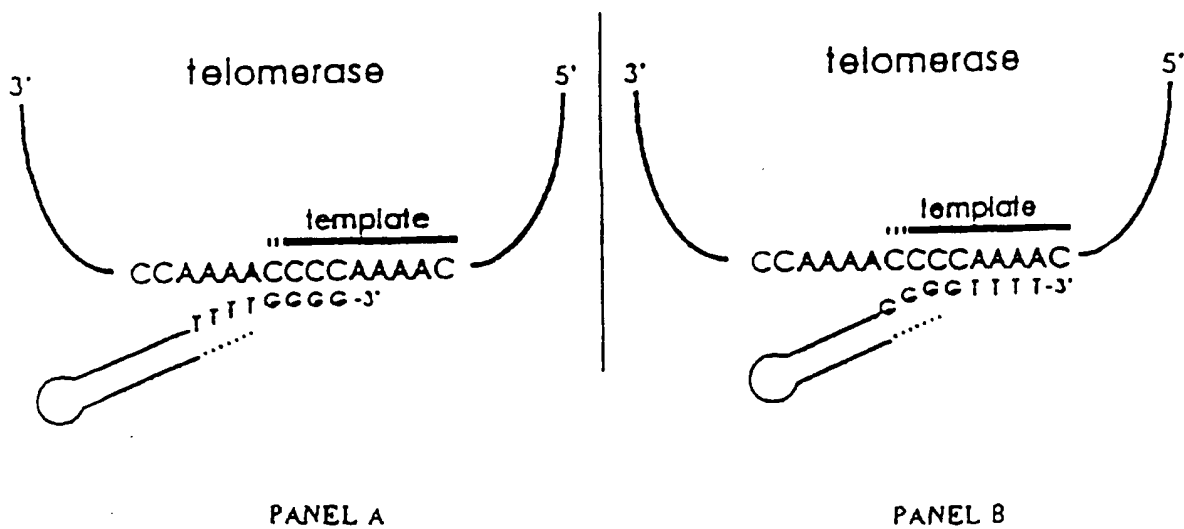




FIGURE 8

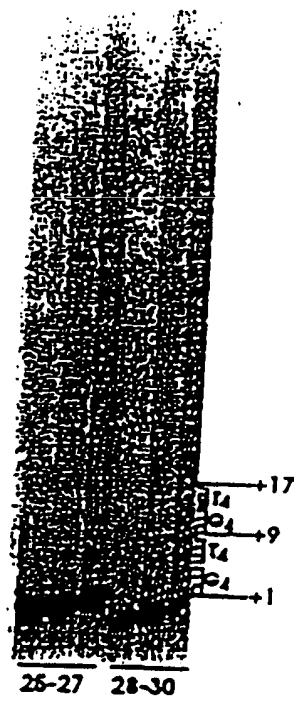


FIGURE 9

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1  AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
51  AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
101  ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
151  TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
201  TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
251  TTAGAAGATA TTAAATATT TCGCAGACA AATATTGTTG CTACTCCACG
301  AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
351  CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT
401  TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
451  ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
501  CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551  ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
601  GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
651  ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701  GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
751  GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
801  ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
851  AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
901  AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
951  GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001  CTGAGAAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051  TCCTCTTCCA GAAAATTGGC GGGAACGGAA AAAAAAATC GAAAACCTGA
1101  TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151  TACACAACCTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA
1201  CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251  AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTAC
1301  AAAAATTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351  GGTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
1401  ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451  CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501  AACCTATTAC TACAGAAAGA ATATTTGGA CGTCATTATG AAAATGTCAA
1551  TCGCAGACTT AAAGAAGGAA ACGTTGCTG AGGTCCAAGA AAAAGAGGTT
1601  GAAGAATGGA AAAAGTCGCT TGGATTGCA CCTGGAAAAC TCAGACTAAT
1651  ACCGAAGAAA ACTACTTTC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701  TAAATTCAGA CCGGAAGACT ACAAATTA CTACAAATAC GAAGTTATTG
1751  AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801  TTTTGATTCT GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851  AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAACT CTCTTTGCA
1901  ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAATCTATC
1951  AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTT TGGATTATGA
2001  CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051  TTTAGAAAAG AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101  TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAAATG
2151  AACAAAATGA CTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201  AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251  CCAATATAAT TACATTAAT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301  GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

```

## FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA  
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC  
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT  
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA  
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA  
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC  
2651 TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT  
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT  
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC  
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT  
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG  
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC  
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA  
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG  
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA  
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA  
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA  
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGG TCTTATATAC  
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD  
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGGA  
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWWNMKSRTR IFYCTHFNRN  
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAM  
301 LEKVKDFNEN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS  
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHLEIH  
401 KNLLLEKINT REISWMQVET SAKHFYFDH ENYVLWLL RWFEDLVVS  
451 LIRCFYVTE QKSYSKTTY YRKNIWDVIM KMSLADLKE TLAEVQEKEV  
501 EEWKKS LGFA PGKRLIPKK TTERPIMTFN KKIVNSDRKT TKLTTNTKLL  
551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA  
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN  
651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLLIVEAKQ  
701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY  
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIKEL  
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI  
851 SIDMKTLALM PNINLRIEGL CTLNLNMQT KKASMWLKKK LKSFLMNNIT  
901 HYFRKTTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID  
951 LEVSKIYYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIIEFSTK  
1001 KYTFNRVCM I LKAKEAKLKS DQCQSLIQYD A

FIGURE 11

```

1  CCCCCAAACC CCAAACCCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG
51 GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
351 AATCAGGTAA TGAGGATTAT TCTATTTTT AGATCACTTC TTAAGGAGCA
401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT
451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTAATTTCG
601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
651 TTGAGACAAT TGAAAAAGCT GTTTACAAC TGAAGGAATCG CAGTTCTGAA
701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
801 TAATGGAATA TACGTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
851 TTGGATTCTT AAAGCATAGA TACACAGAA TCTTTAGAGA CTGATTTAGC
901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001 TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051 AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101 AGGTAAGAGA GATACATTCA TTTAAATTCA TATATTATAG TTTTTCATT
1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAA
1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
1751 GGGGTTTTGG GG

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FIGURE 12

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CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAAATTCAGGTAGTTTGA
60
GGCGTTTTCGGCTTTTCGGCTTTTCGGGATATTTTCTTTTAACTCCATCAAAATCT
A
P Q N P K T P K P L . K K K K L R . F R .
D
P X T P K P Q N P Y K K R X N C G S L E .
C
P K P Q N P K T P I K K E K I E V V . K .
AATAAAATATTATCCCGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT
61
TTATTTTATAATAAGCGCTTTTACCTCTACCTATAACTAAACCTACTATATCTTTAA
120
N X I L F P H K W R W I L I W H I . K I .
D
I X Y Y S R T N C D C Y C F C C Y R K F .
C
N I I P A Q M E M O I D L D D I E N L .
TACTTCTAATACATTCAACAAGTATAGCAGCTCTGTAGTGACAAGAAAGGATGCAAAA
121
ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAATCACTGCTTCTTCTACGTTTT
180
Y F L I H S T S I A A L V V T R K D A K .
D
T S . Y I O Q V . O L L . . O E R H Q N .
C
L P M T F N K Y S S S C S D K K Q C K T .
CATTGAAATCTCGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
181
CTAACTTTAGACCGACCTTTAGCGGAAGTAACTGATAAGGTTTCAAGGTTTTGTTAATC
240
H C N L A R N R L H C L F O S C X N N . .
D
I E I W L E I A F I D Y S K V A K T I R .
C
L X S G S K S P S L T I P K L Q K Q L E .
AGTTCTACTTCTCGGATGCAAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTAA
241
TCAAGATGAAGACCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT
300
S S T S R H O I F I T I L S C E N . . F . .
D
V L L L G C K S L . R F F L E K I S F K .
C
F Y F S D A N L Y N O S F L R K L V L K .
AAACCGGAGACCAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
301
TTTGGCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTACTCCATT
360
K A E S X E . X L X H Y . C L N K I R . .
D
K R R A K S S N C N I T N V . I X S G N .
C
S Q E Q R V E T E T L L H F K . N O V M .
TGAGCATTTATCTATTTTATGATCACTTCTTAAGGAGCATTATCGAGAAAATTACTTAA
361
ACTCCTAATAAGATAAAAAATCTAGTGAAGAAATTCCTGTAATACCTCTTTTAAATGAATT
420
C G L F Y F L D H F L R S I M E K I T . .
D
E D Y S I F . I T S . G A L W R K L L N .
C
R I L L F F R S L L K S H Y G E N Y L I .
TACTAAAGGTAAACAGTTTCGATTATTTCCCTAGCCAACAATGATGACTATATTAATT
421
ATGATTTTCGATTGTCAAACTAATAAAGGGATCCGTTGTTACTACTCATATAATTAA
480
Y . X V H S L D Y F P S O O C C V Y . I .
D
T K R . T V W I I S L A N N D E Y I X F .
C
L K G X O F C L F P . P T H H S I L N S .

```

FIGURE 12 (cont.)

```

CATATGACAATGAGTCAAAGGATCTCCGATACATCAGACTTACCAAAGACAACTCGGTAT
481 ----- 540
GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATCGTTTCTCTTTGACGGATA

a H H R M S O R I S I H O T Y O R O T R Y
b I C E C V K G S R Y I R L T K O K L A I
c Y E N E S K O L D T S O L P K T N S L

AAAAAGCAAGAAAAAGTTTGATAATCGAACACGAGAAGAACTTATTGCATTTACTATTTCG
541 ----- 600
TTTTCGGCTTCTTTTCAAACATTAGCTTGTCGCTTCTTGAATAACGTAATGATAAGC

a K T O E K V C S H S R R T Y C I Y Y S
b K R K K K F D N R T A E E L I A F T I R
c N A R K S L I I E O O K N L L H L L F V

TATCGCTTTTATTACAATTCTTTAGGTATCGACGGTGAACCTCCGAGTCTTGAGACAAT
601 ----- 660
ATACCCAAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a Y G F Y Y N C F R Y R R C T P E S C D N
b M G F I T I V L G I D G E L P S L E T I
c W V L L O L F V S T V N S R V L R O L

TGAAAAAGCTGTTTACAACGAAGGAATCGCAGTTCTCAAAGTTCTGATGTATGCCAT
661 ----- 720
ACTTTTTCGACAAATGTTGACTTCTTAGCGTCAAGACTTCAAGACTACAGATACGGTA

a C K S C L O L K E S Q F C K F C V C H
b E K A V Y M C R N R S S S E S S O V Y A I
c X K L F T T E G I A V L K V L H C H P L

TATTTTGTGAATTAACTCTCAAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721 ----- 780
ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a Y F V M S O I S Y L N L H D S Y R N K
b I L C I N L K Y L I S I W I A I E T N
c F C E L I S H I L S O F N G L K O T

CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCTTTGGGACAAATGCACAC
781 ----- 840
CGTTTATTTGCTACGTTCAAATTACCTTATATGCAATTTAGGAAACCGCTGTTTACGCTGC

a P N X P C K F N C I Y V K S F G T N A H
b O I N H A S L H E Y T L N P L G O M H T
c T T O V M N I R I L W O K C T L

TGAATTTATATTGCAATCTTAAGCATAGATACAGAAATGCTTTAGAGACTGATTTAGC
841 ----- 900
ACTTGAATATAACCTAAGCAATTTCTATCTATGCTCTTACGAAATCTCTGACTAAATCG

a C I Y I G F L K M R Y T E C F R D C F S
b E F I L D S S I O T O N A L E T O L A
c N L Y I L K A I H R H L R L I L

TTACAACAGATTACCTGTTTTCATTACTCTTGCTCATCTCTTATATCTTTAAAGAAGCA
901 ----- 960
AATGTTGCTCTAATGACAAAACTAATCAGAACGAGTAGAGAATATAGAAATTTTCTTCT

a L O O I T C F D Y S C S S L I S L K E A
b Y N R L P V L I T L A H L L Y L K K O
c T T O Y L F C L L L L I S Y I F K R S R

CGCCAAATGAAAAGAACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAAAC
961 ----- 1020
CCGCTTTACTTTCTCTGATTCTTTCTTAAAGTTTAAACAACCTAAGAAGACATTGG

a G E H K R R L K K E I S K F V D S S V T
b A X C X E D R R R F O N L L I L L P
c R N E X N T X E R O F K I C C F F C N R

GGAATTAACAACAAGAAATTAGCAACGAAAAAGAACAGCTATCACAAATCCTGATTC
1021 ----- 1080
CCTTAATGCTGCTCTTAACTCTTCTTCTTCTTCTCGATAGTGTAGGACTAAG

a C I N H X N I S N E K E E L S O S C F
b E L T T R I L A T K K K K S Y H N P O S
c N O O E F O K R R R A I T I L I L

```

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FIGURE 12 (cont.)

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1081  TTAAGATTTCAAAAATTCAGGTAAGAGAGATACATTCAATTAATTCATATATTATAG 1140
      AATTTCTAAAGTTTTTAAGGTCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

A    L K I S K I P G K R D T F I K I H I L .
D    R F O K F O V R E I H S L K F I Y Y S .
C    K D F X N S R . E R Y I H . N S Y I I V .

      TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTCATTAGCTGGAA
1141  ----- 1200
      AAAAAGTAAAGTCTCGACAATAAAAGAAAAATAGAATTGTTATAAAAAACTAACTGACCTT

A    F F I S O L L F S F I L T I F F D . L E .
D    F S F H S C Y F L L S . O Y F L I S W K .
C    F H F T A V I F F Y L N N I F C L A G S .

      GTAAAAAGTATCAATAAGAGAAGCGCTAGACTCAGGTAACCTTAGCTTATTCACATTCAT
1201  ----- 1260
      CATTTTTCATAGTTTATTTCTCTTCGGATCTGACTCCATTGAATCGAATAAGTCTAAGTA

A    V K S I K . E K R . T E V T . L I H I H .
D    K V S N K R S A R L R . L S L F T F I .
C    K X Y O I R E A L D C G N L A Y S H S .

      AGATCGACCTTCATATATCCAATACGATGATAAGCAACAGCAGTCATCCGTTTTAAAAA
1261  ----- 1320
      TCTAGCTCGAAGTATATAGGTTATGCTACTATTCTTTCTGCTCAGTAGGCAAAATTTT

A    R S T F I Y P I R C . G N S S H P F . K .
D    O R P S Y I Q Y D O X E T A V I R F K N .
C    I D L H I S N T H I R K O O S S V L K I .

      TAGTCTATGAGGACTAAATTTTATAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAA
1321  ----- 1380
      ATCAGGATACTCTGATTTAAAAATCTCAGTCTTTACCTCGGCTTTAGAATTAGTTTT

A    C Y E D . I F R V K K W S R N L N O K .
D    S A H R T X F L E S R N G A E I L I K K .
C    V L C G L N F . S O E H E P K S . S K R .

      GAATTGCGCTCGATATTGCAAAAGAATCGAACTCTAAATCTTTGTTAATAAGTATTACCA
1381  ----- 1440
      CTTAACCAGCTATAACGTTTTCTTAGCTTGAGATTAGAAAGCAATTATTCATAATGCT

A    E L R S Y C K R I E L . I F R . V L P .
D    N C V D I A X E S N S X S F V N X Y Y O .
C    I A S : L O X N R T L N L S L I S I T N .

      ATCTTGATTGATTGAAGAGATTGACGAGGCACTECACAGAAGATCATTAAAGAAATAAA
1441  ----- 1500
      TAGAATTAACCTAACTTCTAACTGCTCCGTTGACGTGCTTCTAGTAATTTCTTTATTT

A    I L I D C R D . R G N C T E D H . R N X .
D    S C L : E E I D E A T A O K I I X E I X .
C    L D C L X R L T R O L H H R R S I X K . S .

      GTAACTTTTATTAATTAGAGAAATAAACTAAATTAATAATAGAGATCAGCGATCTTCAA
1501  ----- 1560
      CATTCGAAATTAATTAATCTCTTATTGATTAAATGATTATATCTCTAGTCCGTAGAAGTT

A    V T F I N . R I N . I T N I E I S D L O .
D    L L L I R E . T K L L I . R S A I F N .
C    N F Y . L E N K L N Y . Y R O O R S S I .

      TTGACGAAATAAAAGCTGAAGTAAAGTTACACAATAAAAAATACAAAGCTTCGTCAAAAT
1561  ----- 1620
      AACTGCTTTATTTTCGACTTGATTCAATCTGTTATTTTATGTTTGAACCACTTTTA

A    L T K . X L N . S . T I X N T N L G O N .
D    C R N X S C T K V R O . K I O T L V K I .
C    D E I X A E L K L O N K K Y K P H S X Y .

      ATTGACGAGGAAAGCAAGACCACTTAGCAAAAGAAAAATAAGGCAATAAATAAAATGA
1621  ----- 1680
      TAACTCCTTCCTTTCTCTGCTCAATCGTTTTCTTTTATTCCGTTATTTATTTACT

A    I E E G X E D O L A K E X I A O . I K C .
D    L R K E X X T S . O K X K . G N X . M E .
C    C G R X R R P V S X R X N X A I V K H S .

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FIGURE 12 (cont.)

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      CTACAGAAGTGAACAAATAAAAGATTATTTTTTTCAATAATTTATTGAAAAGAGGGCTT
1681 ----- 1740
      CATGCTTCACCTTCTTTATTTTCTAAATAAAAAAGTTATTAATAACTTTTCTCCCAA

a      V Q K C R N K R F I F F N N L L K R G V .
b      Y R S E E I K D L F F S I I Y C K E G F .
c      T E V K K . K I Y F F Q . F I E K R G F .

      TTGGCGCTTTTGGCGTTTGGCG
1741 ----- 1762
      AACCCCAAAACCCCAAAACCCC

a      L G F W G F G .
b      W C F C V L G .
c      G V L G F W .

```

FIGURE 13

```

2  EVDTQHOADNHGHSALKTCCEI KEAKTLYSWIOKVIRCRNOSOSHYKDL 51
19 ELELEMOENONDIQVRVK... IODPKOY... LVNVTAACLLOEGSYTOOK 62
52 EDIXEFAOTNIVATPRDYNEEDFKVIARKEVF. STGLHIELIDKCLVELL 100
63 OERRVDTKALL... EVAESDPEFICOLAVYIRNELYIRTITTYIVAF. 107
101 SSEDMSDROKLOCFGFLKGNOLAKTHLLTALSTOKOYFFODEMNOVRAH 150
108 CVMKNTOPFIEKYFNKAVLLPNDLLEVCEFAOVLYI 144
151 IGMELFRHLYTKYLI FORTSECTLVQFCGNNVFDHLKVNDKFDKKOKGGA 200
145 FDATEFKNLY... LDRILSODIRKELTPRKCLQRCVRSKF 181
201 ADMNE PRCCSTCKYNNVNEKDHFLNNINVPMMMKSRTRIFYCTHF 247
182 SEFNEYOLGKYCTES... ORKXTHFRYLSVTNKOKWDOTKKK... 220
248 NRMNOFFKKHEFVSNKWNISAMDRAQTI FTNIFRFMRIRKKLKOKVIEKI 297
221 RKENLLTKLOAIKESDKSKRETG... DIMNVEDAIKALKPAVMKKI 264
298 AYHLEKXKDFNPNYYLTXSCLPENWRERKOKIENLINKTREESKYEE 347
265 AKRONAMK... KHKKAPKIPNSTLESKYLTTFKD 294
348 LFSYTTONKCVTOFINEFFYNILPKDFLTGAMRNKINFOKKVKKYVELNKHE 397
295 LIKCHISEP... KERVYKILCKKYPKTEEEYKAAPGOSASAPFN. PE 338
398 LIXNOLLEKINTREISWMOVETSAXHFFYPDHENIYVLWKLRLWIFEDL 447
339 LAGAKKIEISKWENELSAKNTAEVWONLISSNOLPYAHLRNLN... 386
448 VVSLRCFFPVTEOKSYSKTYYYRKNIDVINXHSIADLKKETLAEVQE 497
387 ILKAGVSD... 394
498 KEVEEMKSLGFAPGKLRLLIPKRTTFRPINTFNKKIVNSDRKTTKLTNT 547
395 TTHS 398
548 KLLNSHLHLKTLKNRHFKOPFGFAVFNYYDOVMKKYEEFVCKWKQVQOPKL 597
399 IVINX... ICEPKAVENSKH 415
598 FFATHDIEKCYDSVMREKLSTFLKTTKLLSSDFWIHTAQILKRIONIVID 647
416 F PLOFFSATEAVN. EAVTKGFKAKK... RENNNLKGQIEAVKE... VVE 457
648 SKNFRKKEMKDYFRKFOKIALEGGQYPTLFSVLENEQONLNKKT LIVE 697
458 KTOEEKKH... ELEQTEEGEPVKVNEGICQYINSIELAIX 496
698 AKORNYFKKDNLLQPVINICQNYINPCKPYKOTKGIPOGLCVSSILSS 747
497 IAVNNLDEIKCHTAIFSDVSGSHSTSHSGGAKKYGSVRTCLECALVLGL 546
748 FYYATLEESSLGFLRDESHNPNPNVLLNRLTDDYLLITTOENNAVLFI 797
547 HVKORCEKSSFYIFSSPSSOCNKCYLEVOL... 576
798 EKLINVSRENGFRFMKK. LOTSFPPLSPSKFAKYGMSVVEQNIQDYCD 846
577 PGDELAPSHOKLLOEKGLGCG... TDPPECIDEWTKNKTIVO 617
847 WIGISIDHKTALHPNINLRIEGILCTLNLNMOTKKASHMLKKKLKSPH 896
618 NIVILSDMIAEGYSIDIMVCGSSIVNSI... KKYKDEVN 653
897 NNITHYFRKTITTEDFANKTLNKLFIGGYKYHOCAYEKD. HFKKNLAH 945
654 PHIKIF... AVDLGCG... KCLNLGDEFNENNYIKIFCH 687
946 SSHIDLEVSKIIYSVTRAFKYLVCNIKDTIFGEENYPOFFLSTLKHPIE 995
688 SDSI... LKFISAKOGGA... NMVE 706
996 IFSTKXYIFNRVC 1008
707 VI... KNPALOKIG 717

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FIGURE 14

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132 LSTOKOYFFODEMNOVRAHIGNEL.FAHLYTKYLIFORTSE..GTLVQFC 178
1 MSRRMO ..KKPOAPICNETNLOFVLQNLLEVYKSOIENYKTOOOOI 43
179 GNMVTOHLKVNOXFDRKORCGAADHNEPRCCSTCKYMVONEKOHFLNNIN 228
44 KEEDLKLLKFKNOQOQCNQNDODDDEE.....MNSNKQOELLRRVN 84
229 VPMNNKXSRTRIFYCTHFNRRNOFFKKHEFVSNKUNISANDRAOTIFTN 278
85 ..OIKOOVQLIKK...VGSXVERDLNLNEDENKKN 114
279 IFRFNRIRKKLKDKVIEKIATHLEKVKDFNFMYLTKSCLPENMRERKO 328
115 CLSEQOVKEZOLRTITTEOVXYQNLVFNHDYQDLNWSGCHRRHRETGY 164
329 KIENLINKTREEKSKYYEELFSYTTDNKCVTOFINE..FFYNILPKDFLTG 377
165 OTEKWFELSHOOK.....NYVSIYANOKTSYCHWLKDYFNK 200
378 RNRKONFOKKVKKYVELNKHLEIHKQLLLEKINTREISHMOVETSAKHFFY 427
201 NMYDHLNVSINRLE..TEAEFYAFODFSQTIKLTNNSYOTVNTD..... 242
428 FOHENIYVLWKLRLWI...FEDLVSLIRCFYFVTEOQKSYSKTYYYRKN 475
243 VNFDMNLCILALLRFLSLERFNILNIRSSY..TRNQYNFEKICELLETT 290
476 WOVINKHSTADLKKETLAEVOEKEVEENKKSGLCFAPGKRLRIPKXTTFRP 525
291 FAVVFSHR.....HLOGINLQVPCFAFYLVNSSSOISVKDSOLO 330
526 INTFNKKIVNSORKTTKLTNTKLLNSHLKLTLMRMHFKOPFGFAVFN 575
331 VYSFSTDLKLVQ..TNKVQOYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378
576 DDVHKKYEZFVCKWKQVQCPKLF.....FATHDIEKCYDS..VMREK 615
379 NVLLKXVXH..ANLNLVSIPTOFNFQYFVNLQHLKLEFGLEPNILTKOK 426
616 LSTFL.....STTKLLSSDPWINTAQILKRAKNI..VIOKXNFRKKEHK 657
427 LENLLLSIXOSKMLKFLRLNFYTYVAQETSROKILKOATTIKMLKMNKNO 476
658 OYFRONFOXIALECCOYPTLFSVLEN..EONDLNKKTLIVEAKORNYFK 705
477 EETPETKOETPSESTSGHKFFOHLSELTELEDFSVN...LOATOECY 520
706 KONGLOPVENICOYNYINFCKFYKOTKCIPOGLCVSSILSSFPYATLEE 755
521 OSLMKLLIATNKLKXFLSYKYCHERSKHOTFIDLKNI...YETLMN 564
756 SSLCFLRDESNPENPMVNLHLRLTDOYLLITTOENAVLFIKLINVSR 805
565 ..LKRCSTNISMPCNHSYELTN.....XOSTFYKFKLTNLQE 500
806 ENGFKFMHKKLOTSPPLSPSKFARYGHDSVEQNIVOOYCDWIGISIDMK 855
501 LQKAKYTFK..ONEFOFMVKSAKIESSLESLEDIDSLCKSIASCNNLO 648
856 TLALHPNINLRIGILCTLNENHOT..KASHMLKK..KLKSFLLQWITH 901
649 NVNI.....IASLLYPNMIOKNPFNKPULLFFKQFEQLNHNENVSINC 691
902 YFRKT:..TTEOFANETLNKLFISCCYKYHOCAYEKDHFKNLAHSSH 948
692 ILDOHILNSISEPLEKNNKXKAPILKRYLLQYLLDYTKLFTLOQLPEL 741
949 IOLEVSKIITYSVT.....KAPFKYLVCHIKDT..IFGEENY 982
742 NOVYINQOLEELTVSEVHKQVWENHKQAFYEPLCEFIKESSTLOLIDF 791
983 POFPLS..TLXHFIEIFSTKXY..IFNRVCHILKAKEAKLRSDOCOSLTO 1028
192 DONTVSODSIRKXILESISESKYHNYLALNPSOSSSLIKSDNEETIOELLK 840

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## FIGURE 15

4 DIOLDDIENLLPNTFNKYSSSCDKKGCKTLKSGSKSPSLTIPK..... 47  
617 NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIASLLYPNNIQKNP 666  
48 LQKOLEFYFSDANLYNDSFLRKLVLKSGEORVE.....IETLLH 86  
667 FNKPNLLFFKOFELKNLENVSINCILDQHIILNSISEFLEIKKKIKAFIL 716

## FIGURE 16

1 NEMDIOLDDIENL...LPNTFNKYSSSCSDKKCKTKLKSGSKSPS... 42  
491 TELAKIYAVNKNLOETKCHTAIFSDVSCSHSTSHSGGAKKYGSVRTCLEC 540  
43 LTIPKLOKQ...LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL 85  
541 ALVLGLHVXORCEKSSFYIFSSPSSOCNKCYL.EVDLPDELRP SHQKLL 589

FIGURE 17

	Motif A	Motif B
Consensus	h--hDh---h--h	h----hG---Sp
telomerase p123	QPTLFPATMDIEKCYDSVNREKLSFLKTTKL-100-KFYRQTKGIRGCLCVSSILSSFYATLEESSLGPL	
Dong (LINE)	KNRNLHCTYIDYKAFDSIPHSWLIQVLEIYKIN-28-ROLAIKKGIVQGSLSPLWFCCLALNPLSHQLJQNDR	
al S.c. (group II)	FGGSNWPREVDLKKCFDTISHDLIISKELRYISD-26-HVPVGPVRCVQCAPTSPALCNAVLLRLDRRLAGLA	
HIV-RT	LKKKRSVTVLVAGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLFGGWKGSIPAIFQSSMTKILRPFPRXQN	
L8543.12	VLPELYPMKFDVXSCYDSIPRMECHRIKDALIN-68-KCYIREDGLEFESSLSA?IVDLVYDDLLLEFYSEPK	

	Motif C	Motif D	Motif E
Consensus	h--YhDDhh	h-h---K	h-hGh-h
telomerase p123	-14-LRLTDDYLLITTTQENN-0-AVLFIKELINVSRNCFKFNMRRLQT-23-QDYCDWIGISI		
Dong (LINE)	-16-HLIYMDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQPGLRCKT-25-KC-YKYLGFQQ		
al S.c. (group II)	-55-VVRYADDILIGVLGSKN-2-KIIKRDLNFNLS.IGLTINEERTLI-4-ETPARFLGYNI		
HIV-RT	-4-IYQYMDLIVGSHLEIG-1-HRTKIEELRQHLRLWGLTTPDRHQK-0-EPFLWPGYEL		
L8543.12	-8-ILKLADEFLLIISTDQQQ.....VINIKKLAMQFPQKYNARNR-41-IRSKSSKGI		

## FIGURE 18

telomerase p43	LQKQLEFVSSDANLYNDSELRKLVLSGEQRYELETLLM
human La	ICHQDEYVEGDFNLPRDKQKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQDEYVEGDHNLPRDKQKQI.LLDDGWVPLETMIK
Drosophila La	ILRQDEYVEGDANLNPRDKSREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLRQDEYVSEFNFPYDRSLRTTAEK.NDGWVPISTIAT

## FIGURE 19

1 aacicaaata attactaan taatcaacaa gattgataaa aagcagttaa taaaacccaa  
 61 tagatttaai itagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata  
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga  
 181 tatataagtt agggtaaga ttgacgatcc taagcaatat ctctgtaacg tcactgcagc  
 241 atgtttgttg taggaaggta gtactacta agataaagat gaaagaagat atatcatcac  
 301 taaagcactn ctgagggttg ctgagcttga tcttgagttc atctgctagt tggcagctta  
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat ttgtgtgt  
 421 ccacaagaat actcaaccaa tcatcgaata gtacttaac aaagcagtac ttgtccata  
 481 tgactttact gaagcttgtg aattgcata ggttctctat attttgatg caactgaatt  
 541 caaaaatttg taatgtata ggatacttc ataagatat cgttaaggaa tcaatttccg  
 601 taagtgtta caaagatgctg tcagaagcaa gttttctgaa tcaacgaat actaacttgg  
 661 taagtattgc actgaatcct aacgttaaga acaatgttc cgttaccctt cagttaccaa  
 721 caagtataag tgggattaaa ctaagaagaa gagaaaagag aatctctaa ccaacttta  
 781 ggcaataaag gaatctgaag ataagtcaa gagagaaact ggagacataa tgaacgttga  
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc  
 901 catgaagaaa cacatgaagg caccataaat tcttaactct acccttgaat caaagtactt  
 961 gaccncaag gacticatta agttctgcca tatttctgag cctaaagaaa gagtctataa  
 1021 gatccnngt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttgtgtatc  
 1081 tgcatttga cctttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa  
 1141 aacatgggaa aatgaatica gtgcaaaagg caacactgct gaggtttggg ataattta  
 1201 ttaagcaat taactcccat atattggccat gttacgtaac ttgtctaa ctttaaaagc  
 1261 cgggtttta gatactacac actctattgt gatcaacaag attgtgagc ccaaggccgt  
 1321 tgagaatcc aagatgttc ctctcaatt ctttagtgc attgaagctg taatgaagc  
 1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaag gtcaaatcga  
 1441 agcagtaag gaagtgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta  
 1501 aaccgaagaa ggagaattg ttaagtcaa cgaagggaat ggcaagcaat acattaactc  
 1561 catgaactn gcaatcaaga tagcagttaa caagaatta gatgaatca-aaggacacac  
 1621 tgcatttctc tctgatttt ctggttctat gattaccta atgtcagggt gagccaagaa  
 1681 gtatgttcc gttctactn gtctcagtg tgcattagtc ctggttga tggtaaaata  
 1741 acgtttgaa aagttctcat tctacatct cagttacctt agttctcaat gcaataagtg  
 1801 ttaattgaa gttatctcc ctggagacga actccgtctt tctatgtaa aacttttga  
 1861 agagaagga aaacttgggt gtgttactga ttcccttat gattgcatg atgaatggac  
 1921 aaagaataaa actcacgtag acaataicgt tattgtct gatagatga ttgcagaagg  
 1981 atattcagat atcaatgta gaggcagtc catgttaac agcatcaaaa agtacaagga  
 2041 tgaagtataa cctaactta aaatcttgc agttgacta gaaggttacg gaaagtgtct  
 2101 taatctagg gtatgattca atgaaaacaa ctacatcaag atattcggt tgaacgattc  
 2161 aatcttaag ttatttcag ccaagcaagg agagagcaat atgttcgaag ttatcaaaa  
 2221 ctgtccctt caaaaaatag gacaaaagt agtttttga gattcttcta taacaaaaat  
 2281 ctacccccc ttgtttt tatgcatag ccattatga atttaattta ttatctatt  
 2341 atttaagta ctacatagt ttatgtatc cagtctatta gcctatcaa atgattctgc  
 2401 aaagaacaaa aaagattaaa a



## FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL  
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN  
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS  
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK  
KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK  
APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFSDSASAP  
FNPELAGKRMKIEISK TWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNLIKAGV  
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKGGQIE  
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG  
HTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ  
CNKCYLEVLDLPGDEL RPSMQKLLQEKGLGGGTDFPYECIDEWTKNKTHTVDNIVILSD  
MMIAEGYS DINV RGSSIVNSIKKYKDEVNPNIKIFAVDLEGY GKCLNLGDEFNENNYI  
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

## FIGURE 21

1 | tcaatctat taattaataa ataaaaaaaa gcaactaca aagaaatgt caaggcgtaa  
 61 | ctaaaaaag ccataggcic ctataggcaa tgaacaaat cttagtttg taftacaaa  
 121 | tctagaagt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaga  
 181 | ggaggatctc aagcmtaa agttcaaaaa tttagattag gatggaaact ctggcaacga  
 241 | tgatgatgat gaagaaaaca actcaataa atataagaa ttattaagga gagtcaatta  
 301 | gattaagtag caagmtaat tgataaaaa agttgggtct aaggtagaga aagattgaa  
 361 | ttgaacgaa gatgaaaaca aaaagaatgg acttcigaa tagcaagtga aagaagagta  
 421 | attagaacg attactgaag aataggtaa gtattaaat tttagttaa acatggacta  
 481 | ccagtttagat ttaaatgaga gtgggggcca tagaagacac agaagagaaa cagattatga  
 541 | tactgaaaa tggttgaaa tatctatga ccaaaaaat tatgtatcaa ttacgccaa  
 601 | ctaaaagaca tcatattgt gggtggccta agattattt aataaaaaa attatgatca  
 661 | tcttaatgta agcattaaca gactagaac tgaagccgaa tctatgcc ttagattt  
 721 | ttcaacaaca atcaactta ctataatc ttactagact gtaacatag acgttaatt  
 781 | tgataataa ctctgtatc tgcattgtc tagatttta ttactactag aaagattcaa  
 841 | tatttgaat ataagatct ctatataag aaattaatat aatttgaga aaattgggta  
 901 | gctactgaa actatctcg cagtgtctt ttctatcgc cacttaacg gcaattcatt  
 961 | acaagttct tgcgaagcgt tctaattt agttaacicc tcatataaa tttagcgttaa  
 1021 | agatagctaa ttataggat actctctc tacagacta aaattagttg acactaaca  
 1081 | agtccaagat tattttaagt tctataaga attcctctgt ttgactcatg taagctagta  
 1141 | ggctatccca gttagtcta ctacgtct agagaacctt aatgtttac ttaaaaagg  
 1201 | caagcatgct aatcttaatt tagttctat ccttacctaa ttcaatttg atttactt  
 1261 | ttttaatta taacattga aattagatt ttgattagaa ccaaatatt ttgacaaaaca  
 1321 | aaagctgaa aatctattt tgagtataa ataataaaa aatcttaatt tttaagatt  
 1381 | aaactttac acctacgtt ctaagaac ctcagaaaa cagatattaa aacaagctac  
 1441 | aacaataaaa aatctcaaaa acaataaaa tcaagaagaa actcctgaaa cttaagatga  
 1501 | aactccaagc gaaagcaca gtggatgaa attttgat catctctg aattaaccga  
 1561 | gcttgaagt ttacgctta acttgtaagc taccgaagaa attatgata gcttcacaa  
 1621 | actttgat agatcaaca attaaagaa gttaaatat agttacaaat atgaatgga  
 1681 | aaagagttaa atggatata tcatagatc taagaatat tatgaacct taacaatct  
 1741 | taaaagatgc tctttaata tatcaaatcc tcatggaac attctatg aactgacaaa  
 1801 | taaagattc actttata aatttaagc gacttaaac taagaattat aacacgctaa  
 1861 | gtatattt aagtagaac aatttaatt taataacgt aaaaagtcaa aaattgaatc  
 1921 | ttctcatta gaaagctag aagatanga tagtctgc aaatctattg cttctgtaa  
 1981 | aaattaca aatgttaata ttatgccag ttgtctat cccaacata tttagaaaa  
 2041 | tctmcaat aagcccaat tctattt caagcaatt gaataatga aaattgga  
 2101 | aaatgtatc atcaactgta ttctgatca gcataactt aattattt cagaattct  
 2161 | agaaaagaat aaaaaataa aagcattat ttgaaaaga tattttat tacaatata  
 2221 | tctgattat actaaattat taaaacact tcaatagta ctgaattaa attagttta  
 2281 | caataatag caattagaag aattgacgt gagtgaagta cataagtaag tatgggaaa  
 2341 | ccacaagcaa aaagcttct atgaacctt atgtgagtt atcaagaat catcctaac  
 2401 | ccttagcta atagatttg accaaaacac tgaagtgat gactctatta aaagattt  
 2461 | agaattata tctgagtcta agtatcaica ttattgaga ttgaacctta gttatctag  
 2521 | cagtttaatt aaatctgaaa acgaagaat ttgaacatt ctcaagctt ggcacgaaa  
 2581 | aggtgttta gtaaaagcat actataaatt cctctatgt ttaccaactg gtactatta  
 2641 | cgattacaat tcatagatg gtgttaatt taatatag tttaataaa tattaaatat  
 2701 | tgaatttc ttgctatt attgaataa tacaataat agtatttt agtattga  
 2761 | atatttta gttattat tcaatttt aagtaataa ttatttca atcaattt  
 2821 | aaaaaatcg

## FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK  
EEDLKLKFKNQDQDGNNGDDDEENNSNKQELLRRVNQIKQQVQLIKKVGSKVEK  
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR  
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHLNVSINRLETEAE  
FYAFDDFSQTIKLTNNSYQTVNIDVNFDDNNLCILALLRFLLSLERFNILNIRSSYTRN  
QYNFEKIGELLETFVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF  
STDCLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL  
VSIPTQFNDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY  
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED  
FSVNLQATQEIYDSLHKLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNITYETLNNLK  
RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE  
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK  
NLENVSNINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPE  
LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD  
DSIKKILESISESKYHHYLRNLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP  
LCLPTGTYYDYNSDRW

## FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL  
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCBS  
ANVNVTLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK  
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNTNSSFFPYSKILPSSSSIKKLTDLR  
EAIPTNLVKIPQRLKVRNLTQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR  
QSPKERVLFIIIVILQKLLPQEMFGSKKNKGKIKNLNLLLSLPLNGYLPFDSLLKKL  
RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRLIPKJIQTFYCTEISSTVTI  
VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNFNHNSKMRIPKKSNEFR  
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE  
FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN  
TNTGVCLKLFNVVNASRVKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY  
TREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV  
INIKKLAMGGFQKYNANRDKJLAVSSQSDDDTVIQFCAMHIFVKELEVWKSSTMN  
NFHRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF  
KDLSINVTQNMQFHSFLQRIEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSNTS  
KFKDNIIILLRKEIQLQAYIYIYIHVN

## FIGURE 24

<i>Oxytricha</i>	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
<i>Euploies</i>	LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

Motif 0

human	AKPLHWLMSVYVVELLRSPFFYVTETTPQKNR
tez1	ISEIEWLVLGKRSNAXMCLSDFEKRRQIFAEFIYWLNSPIIPILQSFFYITSSDLNR
EST2	LKDFRWLFISD---IWFTKHNFFENLNQLAICFISWLPRLIPKIIQTFFYCTEISSVT-
p123	TREISWQVET-SAXHPYYFDHEN-IYVLWKLRLWIFEDLVVSLIRCFFYVTEQQKSYSK

. . . . .

Motif 1

human	LFFYRKSVMKLSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1	TVYFRKDIWKLRCRPI-TSHKHEAPEKINENNVRMDTQK-TTLPPAVIRLLPKK--HTF
EST2	IVYFRHDTWKLITPFIYEFKTYLVENNVCRNHNSTLS--HFNHSGHRIIPKKSNNEF
p123	TYYYRKNINDVIMKHSI-ADLKKETLAEVQEKEVSEWKKK-LQFAPGKLRLLPKK--TTF

. . . . .

Motif 2

human	RPIVMDYVVGARTFRREKRAERLTSRVKALP-SVLNYERA
tez1	RLITN-LRKRFLIKHGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF
EST2	RIIAIPCRGADEEEFTIYKENHKKWAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123	RPIMTFNKKIVNSDRKTKLTNTKLLNSHLMKLTLEN-RMFKDPPGPAVFNYYDDVHKKY

. . . . .

Motif 3 (A)

tez1	KKDLLKHRMFOR-KKYFVRIDIKSCYDRIKQDLHFRIVKK-KLXDPEPVIRKYATIHATS
EST2	KQRLKPKFNNVLPELYFMKFDVKSCYDSIPRMECHRILKD-ALKNENGFFVRSQYFFNTH
p123	KEFVCKWKQVGQPKLPFATHDIEKCYDGVNREKLSTFLRTKLLSSDFWIHTAQILKRN

. . . . .

FIGURE 26

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA  
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT  
TCTAACTACGTGTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG  
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT  
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG  
TCTTTTTTGGCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGAAAAAT  
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT  
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT  
GCCGCCCAAATGGGTCCAACGATCATCTCATCATCCGCAACTGCTGCGCAAATCAAACA  
ACTTACAGAACCAGTGACAAATAAACAATTCCTTACACAAGCTCAATATAAAATTCCTCTTC  
TTTTTTTCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT  
GAGAGAAGCTATTTTTCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT  
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT  
GAATAGTATTTGCCACCATTGGAAGGGACCGTATTGGACTTGTGCGATTGAGTAGGCA  
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA  
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT  
AAGTTTACCCTTAAATGGCTATTTACCATTGATAGTTTGTGAAAAAGTTAAGATTAAA  
GGATTTTCGGTGGTTGTTCAATTTCTGATATTTGGTTTACCAAGCACAAATTTGAAAACCT  
GAATCAATTGGCGATTTGTTTCATTTCTGGCTATTTAGACAATAATCCCAAAATTAT  
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA  
TGATACTTGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAAGCGTACTTAGT  
CGAAAACAAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA  
AATGAGGATTATACCAAAAAAAGTAATAATGAGTTTCAAGATTATTGCCATCCCATGCAG  
AGGGGCAGACGAAGAAGATTACAATTTATAAGGAGAATCAAAAAATGCTATCCAGCC  
CACTCAAAAAATTTAGAAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA  
TTCTCCAACGCAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT  
TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC  
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT  
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT  
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT  
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT  
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC  
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC  
CAGTCCTAGCCAGGACACATTAATTTTAAAACCTGGCTGACGATTTCTTATAATATCAAC  
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA  
TGCGAAAGCCAATAGAGACAAAATTTAGCCGTAAGCTCCAATCAGATGATGATACGGT  
TATTCAATTTTGTGCAATGCACATATTGTTAAAGAATTGGAAGTTTGGAACATTCAAG  
CACAATGAATAATTTCCATATCCGTTGCAAACTAGTAAAGGGATATTTCGAAGTTTAAAT  
AGCGCTGTTTAAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA  
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTGGAATGTTATAAATCTGC  
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCAATCGTTCTTACAACG  
CATCATTTGAAATGACAGTCAGCGGTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA  
TGAGGTACGATTACCATATTGAATGGATTTTGGAAAGCCTATCTTCAAACACATCAAA  
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR  
VQLRDVSEAEVRQHREARPA LLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR  
AERLTSRVKALFSVLNYERA



## FIGURE 28

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC  
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACC  
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA  
GAGGGTGCACTGCGGGACGTGTGGAAGCAGAGGTCAGGCAGCATCGGGA  
AGCCAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG  
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG  
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC  
GTGCTCAACTACGAGCGGGCGCG

## FIGURE 29

MTEHHTPKSRJLRFLNQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF  
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFEERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV  
STFPNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK  
RTIETSITQNK SARKEVSWNSISIRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLOWIFPRQFG  
LINAQVQQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDHDDEKILS  
YSLKPNQVFAFLRSILVRVFPKLIWGNQRJFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL  
GKR SNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFT  
SMKMEAFEKINENNVRMDTQKTTLP PAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT  
LRPVASILKHLNEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR  
IVKKKLLKDPEFVIRKYATI HATSDRATKNFVSEAFSYFDMVVPFEKVVQLLSMKTSOTLFDVDFDY  
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGI PQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL  
LRVVDDFLFITVNKKDAKKFLNLSLRGF EKRFNFSTSEKTVINFENSNGIINNTFFNESKKRMPFFG  
FSVNMRS LDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN  
YRLGYSMCMRAQAYLKR MKDIFIPQRMFITDLLNVIGRKIWKKLA EILGYTSRRFLSSAEVKWLF  
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF LHRRIAD

ggtagcagattacmccmccmccataagcgaattgcttccicgaacgcctcctaaatctcgggaatattttacaagaactcaataaataaccgaagcaaatccaalatgaaag  
ggtanagigatcgataalamctiammatcggtcgtacccaagatataaggacaaaagaacaacttcccccctaaagacmmtacmmtaamttacmmtcaaatatatttcg  
ggncgcttactmmtaaticgggactggttagctgctacttctagccaaacgcggtggttctaccccgctatnggalaatagctctggagtagctcagagaaatccntacaaatct  
ctgagtagacatlaaagatcattacagtcggtgctatcttataacatggagccttaccttagatgagtcacgcgtcgaatgaggtagtammgttalcaccaacgtmgtccntg  
aaaaggttgataattamgcaaaatcatgctccttagtgggtggaacccggaagmttttgatgcttgcacacgcttagcatgattgagatantcaaaamttctaccatcaca  
ciccmmaacgcggmtamttctatmctantctcatggttcccaaaatgtaicctcgtattagggcmtttccggttacciccttggaatcgiaacmmtcacttccccctaatg  
aataaictaaantagmtcgctataaagtagatagtagagaagatnggtgattcctactcgttaatgtaantagmaaagatactmgtcaaaacamtatagctatcattataaaa  
aaaactcctataaattataaataaactaattcggttcactmmtaataaacgtttagtcagtaggacacmgtcaiaatataatgcttaagtgtaactgttaactgtcaacgtCA  
GACCCAAACACCAATACCCCCAAAGAACGAGGATTTCTCGCTTTCTAGAGAAATCAATATGTATACCTATGTA  
CCTTAAATGATTATGTACAACCTTGTGTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA  
CGCTTGAGAAAGCGATGTACAAACGTCCTTTTCTATTTTCTTCAATTCGACTGTAGTCGGCTTCGACAGT  
AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGtataaamtmgttgatmtttctatcgt  
ggatagctaaatagtggtcagCTAATAGCGAATGTTGTAAACAGATGTTTCGATGAAAGTTTTGAGCGTCGAAGGA  
ATCTACTGATGAAAGGGTTTTCCATGttaggtattcttaantggaatamaccgtcaantactgmtcaagagantamtaaccgataaagAA  
TCATGAAGATTTTCGAGCCATGTCATGTAAACGGAGTACAAAAATGATCTCGTTTCTACTTTTCTCTAAATTA  
CCTTATATCTATATCTTGAGTCAAAAAATTTGGCAACTTTTGTAGAAAATGtaaatccggnaagatggtgcgtacmgtgaaca  
agactgacaagtatagTACGGCAGTGATGCCATTCGTAACCTTTATTAACCAAGGAAGTATTTTGAGGCTCTTC  
CAATGACAAATTAACCTTCGATTTCTGGCATACCACTTTTAAAAATAATGTGTTTGAGGAACTGTGT  
CAAAAAAAGGAAAGCGAACCAATTGAAACATCCATTACTCAAAAAATAAAGCGCCCGCAAGAAAGTTTC  
CTGGAAATAGCATTTCAATTAGTAGGTTTAGCATTTTTACAGGTCATCCTATAAGAAAGTTTAAGCAAGgt  
aactaatacignatccnctataactaantmagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG  
TGGCTTCAATGGATTTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA  
AGTGATTTCACTGGTATCACAGAGTACAGTTGTGCCCAAACGCTCTCCTAAAGGTATACCCTTTAATTGA  
ACAAACAGCAAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTAATGCCCATTAATGA  
CACCACGATGATGAAAAAATCCTTAGTTATCTTTAAAGGCCAACAGGTTGTTTGGCTTTCTTCGATC  
CATCTTTGTTGAGTGTATTTCTCTAAATTAATCTGGGGTAAACCAAGGATATTTGAGATAATATTAAGGg  
tatgtataaaamtaaccaciaaacgamtaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC  
ATTATTTAATGAGTAAATATAAGGtaaatatgccaaamttttaccataaataacaalcagATTTAGAAAATTGAATGGCTAGT  
CCTTGAAAAAAGGTCAAATGCGAAAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAAATATTTGCGG  
AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTATATCACTGAATC  
AAGTGATTTACGAAATCGAAGCTGTTTATTTTGAAGAAATATTTGGAAGCTCTTGTCGCCACCTTTAT  
TACATCAATGAAAAATGGAAGCGTTTGAAAAAATAAACGAGtamttaaagtamtmgtcaaaaagcraatamtcagAACAA  
TGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTTCGTCTATTACCTAAGAAGAATAC  
CTTTCTGCTCTATTACGAATTTAAGAAAAAGATTTCTAATAAAAGtanaamttggicacatgiamcttctactatattag  
cagATGGGTTCAACAAAAAATGTTAGTTCAGTACGAAACCAAACTTTACGACCTGTGGCATCGTACTG  
AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGCTTCTTACT  
TTTAAGAAAGGATCTTCTTAAGCACCGAATGTTTGGtataataatgctgcgancctcarantaatmgcagGCGTAAGAAG  
TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAGCAAGATTTGATGTTTCGGATTGTT  
AAAAAGAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG  
AGCTACAAAAAATTTGTTAGTGAGGCGTTTTCTATTGtaagmtamttcattnggaamtttaacaaatcmttagTTGATAT  
GGTGCTTTTGAAAAAGTCGTGCAGTTACTTTCTAGAAAACTACAGTACTTTGTTGTTGATTTTGT  
GGATTATTGGACCAAAAGTCTCTTGAAATTTTAAAAATGCTCAAGGAACATCTCTGTGCACACATTTGT  
TAAAGtataaccaantnggaatgaataacactaatgaactagATAGGAAATTTCTCAATACCTTCAAAAAGTTGGTATCCCTC  
AGGGCTCAATTTCTGTCTATCTTTTTGTGTCTATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTT  
TACGAAAAAAGAAAGGATCAGTGTGTTTACGAGTAGTCGACGATTTCTCTTTATAACAGTTAATAAAA  
AGGATGCAAAAAAATTTTGAATTTATCTTTAAGAGgttagttagtcttacttaagttcaaccgttaggGATTTGAGAA  
ACACAATTTTCTACGAGCCTGGAGAAAAACAGTAATAAACTTTGAAAAATAGTAAAGGGATAATAAACA  
ATACTTTTTTAAATGAAAGCAAGAAAAAGAATGCCATTCTTCGGTTTCTCTGTGAACATGAGGTCTCTTG  
ATACATGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC  
ATATGGGGAAATCTTTTTTTTACAAAAATCTAAAGtatactgtgaactgaataactgtgacaaataalcaATCGAGCCTTGC  
ATCCTTTGCACAACTATTTATTGACATTACCCCAATTCAAAATTCAAATTTCTTTCTGTGCAATATATATAG  
GCTAGGATACTCTATGTGTATGAGAGCACAAAGCATACTTAAAAAGGATGAAGGATAATTTTATTTCCCC  
AAAGAATGTTTCAATAACGGgttagtactanttaaacgaagaagactaataaccittagATCTTTTGAATGTTATTGGAAGAAAA  
ATTTGGAAGAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTGTCTCTGCAGAAGTCAA

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FIGURE 30 (cont.)

ATGgtacgtgicgggicgagacitcagcaatangacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTT  
TCAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTTCAGTCATTGACTGATCTTATCAAGCCGC  
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAIgticattcaamnatatatacctti  
tantactgggticntaaacaatantactiaagiatagctgacccccaaagcaagcatactataggattctagtaaaatnaaiaicicgtatagtttgatgacngicn  
aiccatactmtaagaaagangacagtggtgctgaciacigccacatgccanaaacgggagtggttaaacaftaaagtaatacagtaggciaaictcmtcattag  
aataaggaaagtggmtctataatgaataatgccgcactaatgcaaaaagacgaagattatctttaaacaagggggattagcataiccgaaaggaaagagagtaatai  
acccagtggttggaagaaagcaaggataamggacaagcncigcagatgacaggctaaattmggtgaccgaattmggtaaaagccccagggtatccatgggtggccg  
gcnngctactgagacgaaagaaactaaggatagttgaatactaatagctcattaatgtcctatataaggmtttttccigacttcaattmgcatgggtgaaagaaata  
gtgtaagccattatggatccgaaatagccaaatcnggttcccaagcggagctaaagaaactatgaagccttatgaggcttcaaaaactcctcctgattaaaggag  
gaaicuccaccgatgaggaaatggatagcnaicagctgctgaggagaagcctaaattmgcaaaaagaaataatcattgggagacatcctngatgaatcagatgcgga  
gagtaicccagcggatccngatgtcaataactctatmctgaaatgtatggtctactgtcgttcgactcctgtagctctacgcagtaagtgaccaagggtacc

FIGURE 31

EST2 pep	FFYCTEISST VTIVYFRHDT WN----KLIT F-----FIVE YFK-TYLVEN	40
Euplotes pep	FFYVTEQOKS YSKTYYYRQN IWDVI-MKMS IAD----LKK ETLA--EVQE	43
Trans of tetrahymen	-----KHKE GSQIFYRKP IWKLVSKLTI VKVRIQFSEK NKQMQNIFYQ	44
Consensus	FFY.TE..K. .S..YYRK. IW...-KL.. ....-F..K .....V..	50
EST2 pep	NVCRNHNSY- ----- TLSNFNHSGM FRIIPKSNNE FRIIPPCRG	79
Euplotes pep	KEVEEWKSL ----- GFAPGK FRIIPQITT FRIIPMTFNKK	78
Trans of tetrahymen	KIQLEENLE KVEEKLIPED SFQKYPQKL FRIIPKGS-- FRIIPMTFLRK	92
Consensus	K...E..... ----- F...GKL FRIIPK... FRIIPMTF.RK	100
EST2 pep	ADEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE	129
Euplotes pep	IVNSDRKTTK LTINTKLLNS HLMKTLRN- -----RMFK -DPFGFAVFN	120
Trans of tetrahymen	DKQKNIK--- LNLNQILMDS QLVFRNLKD- -----ML-G -QKIGYSVFD	130
Consensus	.....K..K LN.N..L..S QL..L..LN- -----... -..IG..VF	150
EST2 pep	FKQRLLMFN NVL----- FRIIPKMFV VKSCYD	157
Euplotes pep	YD-DVMKMYE EFVCKWKQVG QFVFFATMD IEKCYD	155
Trans of tetrahymen	NK-QISEHFA QFIEKWKQKG RFIIPYVTL- -----	158
Consensus	.K-...RF. .F..KWK..G FRIIPKMF.T.D ...CYD	186

## FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK  
S-2: RQH LKR VQL RDV SEA EVR QHR EA  
S-3: AFT FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q  
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS  
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIGURE 33

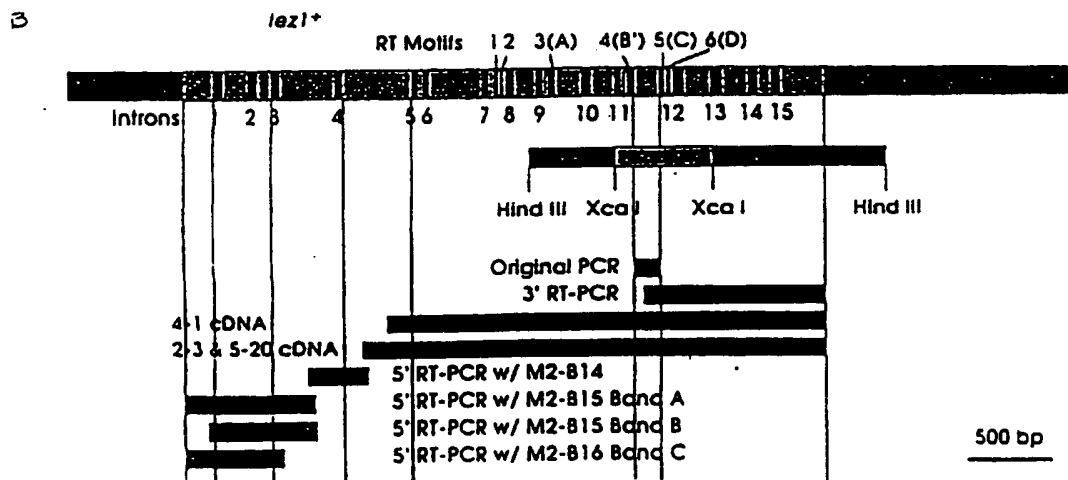
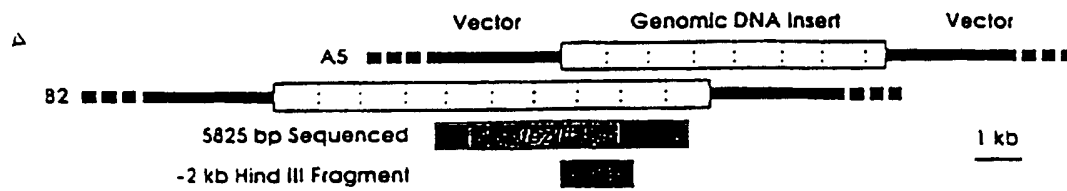


FIGURE 34

Poly 4

			t		t		c		
	t	a	a	g	c	c	t	c	g
5'-	cag	acc	aaa	gga	att	cca	taa	gg	-3'
	Q	T	K	G	I	P	Q	G	

4 (B')

## 5 (C')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	
				t	t	t	t	
						c	c	
						<u>Poly 1</u>		



FIGURE 35

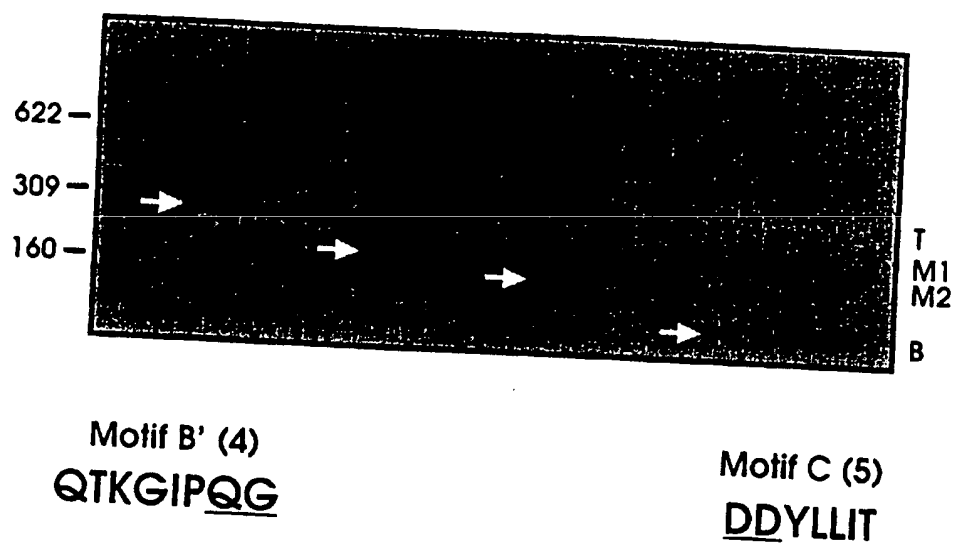


FIGURE 36

# PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

```

Ot                LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123           KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2             SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103           DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
                  . * . * . * . * . * .

```

```

Q K V G I P Q G
caa aaa gct ggt acc cct cag gg..... <---Actual Genomic Sequence.

```

Poly 4

```

      c      c      c
c a a g c c c g
cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca cca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
cc tgg ccc ccc taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

```

```

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

```

```

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

```

```

V V D D Y L L I T

```

```

<---- ctg ctg atg gag gag tag tgg
      a a a a a a a a
              c c c c
              c c

```

Poly 1

```

.....gac gat ttc ctc ttc ata aca..... <---Actual Genomic Sequence.
D D F L F I T

```

411107

FIGURE 37

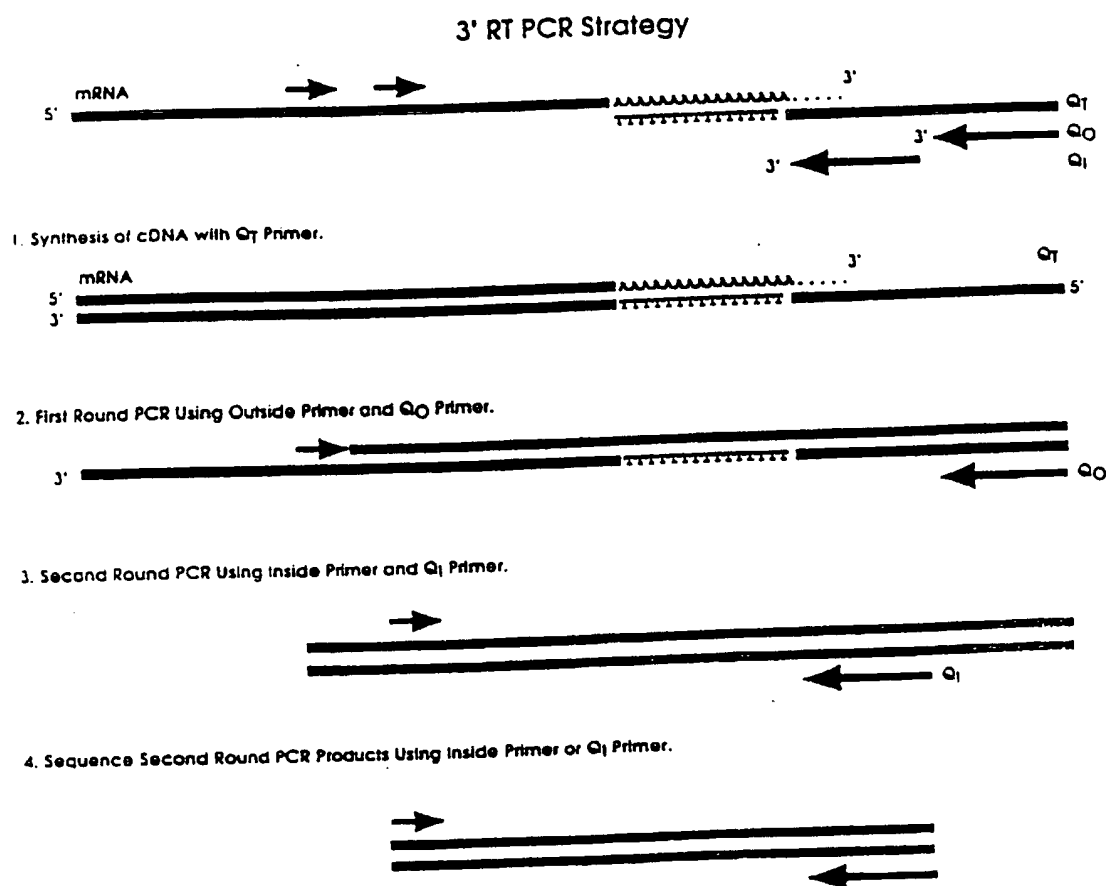


FIGURE 38

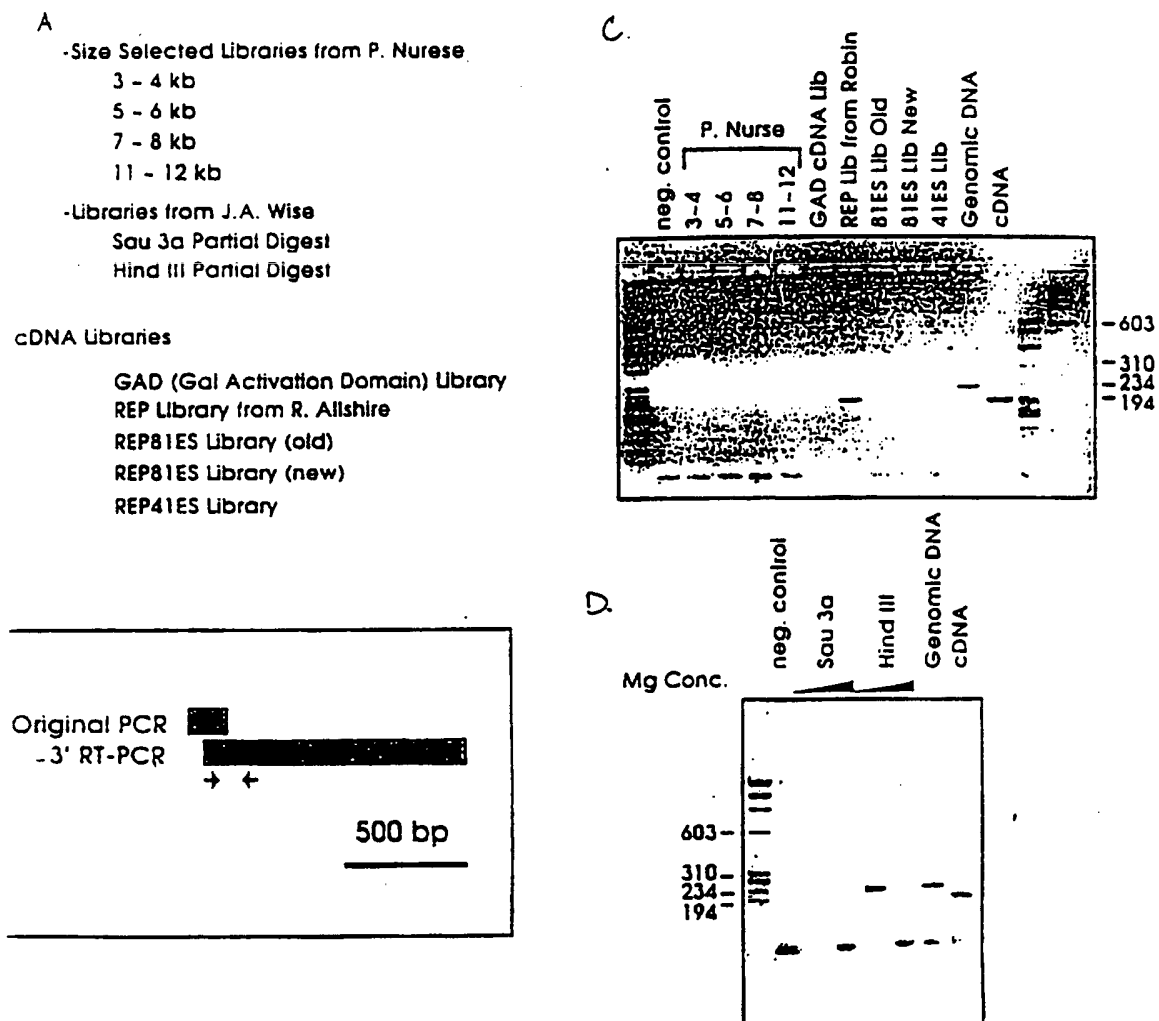


FIGURE 39

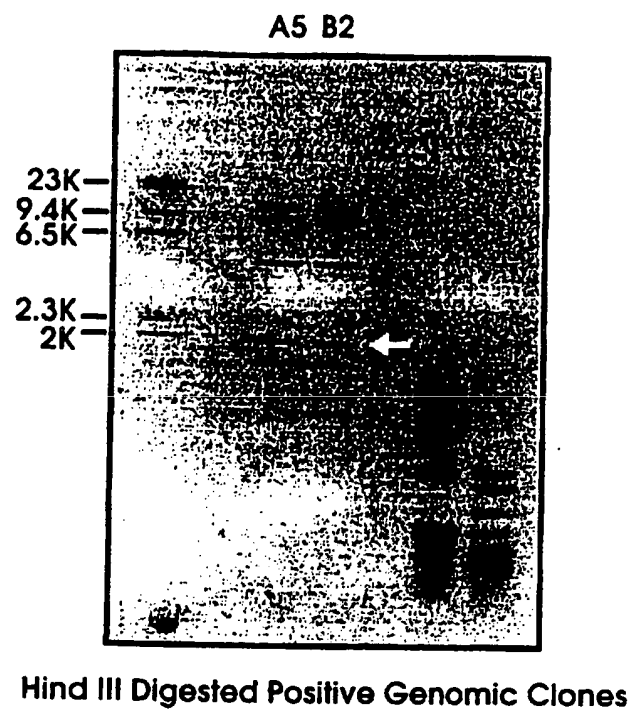
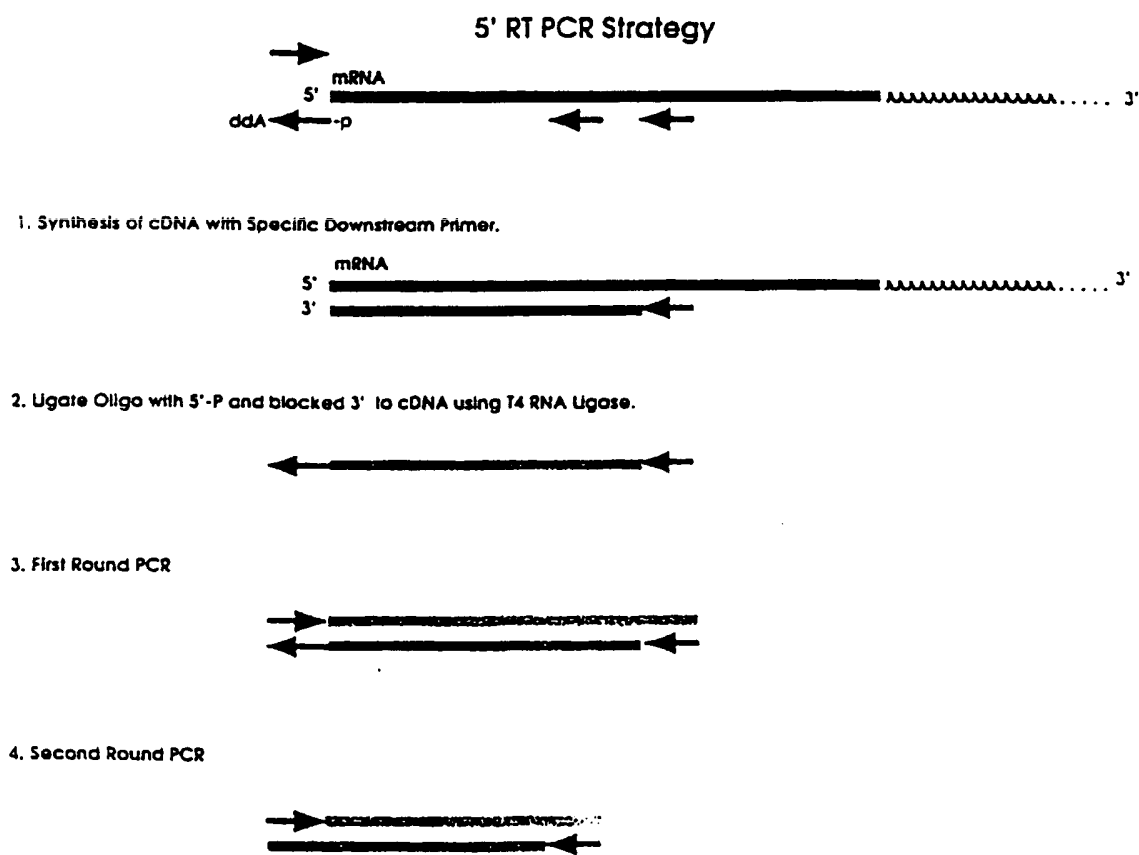


FIGURE 40



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FIGURE 41

## Alignment of RT Domains from Telomerase Catalytic Subunits.

```

                                Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ... (35)...
S.c. Est2p (366). WLFRLQIPKIIQTFFYCTEISSTVT-IVYFRHDTW ... (35)...
E.a. p123 (441). WIFEDLVVSLIRCFYVTEQQKSYSKTYYYRKNIW ... (35)...
      *          *** **          * *
      Motif 1      Motif 2      K
      p hh h K      hR h      R
S.p. Tez1p AVIRLLPKK--NTFRLITN-LRKRF ... (61)...
S.c. Est2p SSMRIIPKKSNNEFRIIAIPCRGAD ... (62)...
E.a. p123 GKLRLLPKK--TTFRPIMTFNKKIV ... (61)...
      *      ***      **
      Motif 3(A) AF
      h hDh GY h
S.p. Tez1p KKYFVVRIDIKSCYDRIKQDLMFRIVK ... (89)...
S.c. Est2p ELYFMKFDVKSICYDSIPRMECMRILK ... (75)...
E.a. p123 KLFATMDIEKCYDSVNREKLSTFLK ... (107)...
      *      *      ***      *
      Motif 4(B')
      hPQG pP hh h
S.p. Tez1p YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ... (6)...
S.c. Est2p YIREDGLFQGSLSAPIVDLVYDDLLEFYSEF ... (8)...
E.a. p123 YKQTKGIPQGLCVSSILSSFYATLEESSLGF ... (14)...
      *      *      *      *
      Y Motif 5(C)      Motif 6(D)
      E F DDhhh      Gh h cK h
S.p. Tez1p VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEXHNFSTSLKTVINFENS . (205)
S.c. Est2p LILKLADDFLIISTDQQQVINIKKIAMGGFQKYNAPANRDKILAVSSQS . (173)
E.a. p123 LLMPLTODYLLITTQENNAVLFIKLINVSRENGFKFMKKLQTSFPLS . (209)
      ** * *

```

Figure 42

*A*

[illegible]



24 Sp\_Tp1p 1 .....MTENI ASRIPLFLENQYVVLCT 24  
 25 Sp\_Ea2p 1 .....MKILFEP 25  
 26 Sp\_p123 1 MEVDVDRGADRHGIMSAKTCESIKKATLYSW 26  
 27  
 28 Sp\_Tp1p 11 LHOYVQLVLRGSPA 11 SNICERLASDVOTSPS 11  
 29 Sp\_Ea2p 11 IODELDIDLOTH 11 T K ...ENLACOMFNOLD 11  
 30 Sp\_p123 11 IGVIRGRHSG 11 T K ...OLEDIKIFAOTM 11  
 31  
 32 Sp\_Tp1p 31 IFLNSTYVVOFDEKPOEGVOPSSPKCSOSELAN 31  
 33 Sp\_Ea2p 31 KILTYCPALPHRR-KIALPCLPOLSLNKAIVOM 31  
 34 Sp\_p123 31 IYATPPOVREEDPRVIARKEVPSTGLNLSLMDK 31  
 35  
 36 Sp\_Tp1p 51 VYKMPDESFERRR-NLLMKPSMNHEDFRAMN 51  
 37 Sp\_Ea2p 51 CIIYLLTGLLYM...NVLTPYKIARNED 51  
 38 Sp\_p123 51 GLVELLSDDVDSDRDKLGGPFPOLKQNG 51  
 39  
 40 Sp\_Tp1p 112 VNGVONOLVSTPPNYLISILSEENQLLEI 112  
 41 Sp\_Ea2p 112 ---VNSLFCNBNVYVTLKGAAMKMFSLV 112  
 42 Sp\_p123 112 ---LAKTHLLTALSTORGYFFOENOVNAMI 112  
 43  
 44 Sp\_Tp1p 150 SOAMNYLSKQSIPEALPHNHYLS 150  
 45 Sp\_Ea2p 150 TYAFVONLINTYVIGPN-GOPFTIVNRRCKEP 150  
 46 Sp\_p123 150 NELPNNYTKYLIFORTSEGLYVFCNNVVDN 150  
 47  
 48 Sp\_Tp1p 180 NVFSEYVKKERTIETSIYON...SKARKE 180  
 49 Sp\_Ea2p 180 MLPPRWVO--RSESSATAAQI...KOLYSPET 180  
 50 Sp\_p123 180 LKYNDRPDK-KQGGAAAMRPRCCSTCKYMK 180  
 51  
 52 Sp\_Tp1p 210 WWSISIRFSIFVNSYKPKQDLVFNLSICD 210  
 53 Sp\_Ea2p 210 N...KPLMKLNINSSSFPF 210  
 54 Sp\_p123 210 NEK--DNPLNNINVPNNNNRSTRIFYCTHFN 210  
 55  
 56 Sp\_Tp1p 240 RNTVHWLOWIPROFGLNAPGVKQLNXYPL 240  
 57 Sp\_Ea2p 240 ---YSKILPSS...SIKELTOLREAFP 240  
 58 Sp\_p123 240 R...NHOFFKHEFVSNKNNISAMDRAOTI 240  
 59  
 60 Sp\_Tp1p 270 VS...GSTVVPKRLLEVPPLIGOTAKRLNRIS 270  
 61 Sp\_Ea2p 270 TN...LVKIPORLEVRINLTLOKLLRNKALN 270  
 62 Sp\_p123 270 PTNIPFNRIRKRLKORVIERIATVLEKVDPN 270  
 63  
 64 Sp\_Tp1p 300 LSKVYNNHYVID-THODEKILSYBLEPNO 300  
 65 Sp\_Ea2p 300 YVSLNDIDPLEQTVLDLNLSSRSPKER 300  
 66 Sp\_p123 300 FNYLTESLPLENWRERKOKIENLNKTRK 300  
 67  
 68 Sp\_Tp1p 330 .....LALSLVLYVPKLI 330  
 69 Sp\_Ea2p 330 .....LILVILDKLLQSM 330  
 70 Sp\_p123 330 SKVTESELPVYTONKCTG...INEFPYHILKOP 330  
 71  
 72 Sp\_Tp1p 360 WNGRIFPILILETFLKRYVESPLNHYMS 360  
 73 Sp\_Ea2p 360 POSKRRKOKIILNLLLSPLNOYLPPDSLK 360  
 74 Sp\_p123 360 LIG-ANRRNPOKRYKRYVEMKHELINHEML 360  
 75  
 76 Sp\_Tp1p 390 NIKISEIELVLOKRNHAKMCLDPPKRRKIFA 390  
 77 Sp\_Ea2p 390 KRLKDPNHLFIS...DIWPTNNPNNLHOLA 390  
 78 Sp\_p123 390 KHTYRISMMOVETS-AKMPYVPOHNN...IYVLV 390  
 79  
 80 Sp\_Tp1p 420 EPIYLYNAPFIPILGSI...ISDLDNRVTY 420  
 81 Sp\_Ea2p 420 CFISLFRQLIPKIIOT...CPISESTYV-IVN 420  
 82 Sp\_p123 420 KLLNIFEDLVSLINC...VVOGRSYSEKTY 420  
 83  
 84 Sp\_Tp1p 450 PKDINKLLCRPPITSMKMEAPKINENNVMD 450  
 85 Sp\_Ea2p 450 PMNDTINKLITPPVEYFETVLYNRRVCRNHS 450  
 86 Sp\_p123 450 YKNNIDVYIMKMLADLKESYLAEOEKREVEW 450  
 87  
 88 Sp\_Tp1p 480 TOKTYLPPAVILL...NTLTLNLRKPL 480  
 89 Sp\_Ea2p 480 TYLBNPNNHKKI...NNHNE...IAPICROAD 480  
 90 Sp\_p123 480 KKSLOPAPORLML...TY...MTFNKKIV 480  
 91  
 92 Sp\_Tp1p 510 IKNSKNEKMLVSTNOTLRPVAAIKHIE 510  
 93 Sp\_Ea2p 510 CEE...FYIVKRNENAIOPTOKI...EYAKRPT 510  
 94 Sp\_p123 510 NSD...KTYTLTNTKLLNSHLMKTKRR-MF 510  
 95  
 96 Sp\_Tp1p 540 EESGIPPHLEVVMKLLTPKKDLLNRMFOR-KK 540  
 97 Sp\_Ea2p 540 SRTKIVSTQIADRIKPKORLLKPNHVLPEL 540  
 98 Sp\_p123 540 EDPPGPAFVNYDGYMKKYESPYCKWGOVGPAL 540  
 99  
 100 Sp\_Tp1p 570 YVRIKESRIKODLMFRIYKLLKDPF 570  
 101 Sp\_Ea2p 570 YMEPEVESGSIIPNHECMRILDAKLNEN 570  
 102 Sp\_p123 570 IATYIKESVYNNKELSTFLTYKLLSSD 570  
 103  
 104 Sp\_Tp1p 600 VIRKVTINATSDRATEN 600  
 105 Sp\_Ea2p 600 FVRSQVFFNTYTG 600  
 106 Sp\_p123 600 WIMTAQILKRNHIVIDSKNPKKKNKDYPROK 600  
 107  
 108 Sp\_Tp1p 630 FVSEAFSYFDMVPPFKVOLL...NKYSDTFV 630  
 109 Sp\_Ea2p 630 .....VLELNNVNASR...VPKPYEYVI 630  
 110 Sp\_p123 630 FQKIALEGGYPTLP...LENSONOLNAKKTIV 630  
 111  
 112 Sp\_Tp1p 660 OPVQVYTKESSEIFKMLKEHLNIVEIGNSO 660  
 113 Sp\_Ea2p 660 ONVRYVNLHGQDVINUVNEIFKTLWVEDECH 660  
 114 Sp\_p123 660 EAKORNTVPRKORLLGPVINGOVYVINYHOKP 660  
 115  
 116 Sp\_Tp1p 690 LQV...IP...SILSPLCHPYMEOIDVLSYTK 690  
 117 Sp\_Ea2p 690 IRCDLP...SLLAPIVDLYTDOLEFYSEKA 690  
 118 Sp\_p123 690 KQTR...IP...LCV...SILSOPVYATRESSELOLR 690  
 119  
 120 Sp\_Tp1p 720 KKG...SVLLRV...PTNNKKDARK 720  
 121 Sp\_Ea2p 720 SPQSD...TLIKEL...ISTOQOQVIN 720  
 122 Sp\_p123 720 GEMNPEKPHVLLMLRL...TYOENNAV 720  
 123  
 124 Sp\_Tp1p 750 FLNLSLQPKNNPFSYLSVIVINPENN 750  
 125 Sp\_Ea2p 750 IRELANOGOPORVNAHARRDILAVSSD 750  
 126 Sp\_p123 750 FIKLINVSRENHPPNNMLLOTSPPLPKPKFA 750  
 127  
 128 Sp\_Tp1p 780 ---INHTFPNRESKRNPPFPVNNRSLDTLL 780  
 129 Sp\_Ea2p 780 ---DOTVIOPCA...NNIFVKELEVNNSSBM 780  
 130 Sp\_p123 780 KYQMSVSEONIVDGYDWDIGISOMKTLALMP 780  
 131  
 132 Sp\_Tp1p 810 ACPKIDGALFNSTREVELTKHNGKSPFFILRS 810  
 133 Sp\_Ea2p 810 NMPHISSESSKGIPLSLIALNTRISYTIOTN 810  
 134 Sp\_p123 810 NINLRISGILCTLNLHMOYKASWLEKLNKSP 810  
 135  
 136 Sp\_Tp1p 840 ASFAGVFDITNHSKPNSSCNIVRLQVSNMCR 840  
 137 Sp\_Ea2p 840 NSTHTVLSQIDHNVKHSIED 840  
 138 Sp\_p123 840 NNNITNVPRETYTTEPANKYLNELPISGOVE 840  
 139  
 140 Sp\_Tp1p 870 AOAYLEK...IP...PNNFIDLLNVIKRWKK 870  
 141 Sp\_Ea2p 870 ---VKSAP...VTRNMOPHSFLORTEM 870  
 142 Sp\_p123 870 YMOGAKETN...KKNLANSSHIDLSVKIETSV 870  
 143  
 144 Sp\_Tp1p 900 LAEILGYTSRRPLSBAEVKWLFCLOMRDOKPS 900  
 145 Sp\_Ea2p 900 TVSGQPIITGQPLLEYEVVPTILNDFLSSBN 900  
 146 Sp\_p123 900 TRAFFKVLCHNISTIFGSENVDPFPLSTKMF 900  
 147  
 148 Sp\_Tp1p 930 FRYHPPGEGLIYV...SLTDLIKPLRPYRQVLF 930  
 149 Sp\_Ea2p 930 S...EDDILKRIKSIOMQAVI 930  
 150 Sp\_p123 930 ISIPS...TKKVI...RVCMLKAKAKKESDGC 930  
 151  
 152 Sp\_Tp1p 960 LHRRIAG 960  
 153 Sp\_Ea2p 960 IYINIVL 960  
 154 Sp\_p123 960 QSLIOYDA 960

B Figure 42

Fig. 42

FIGURE 43

Disruption strategy for the putative telomerase genes.

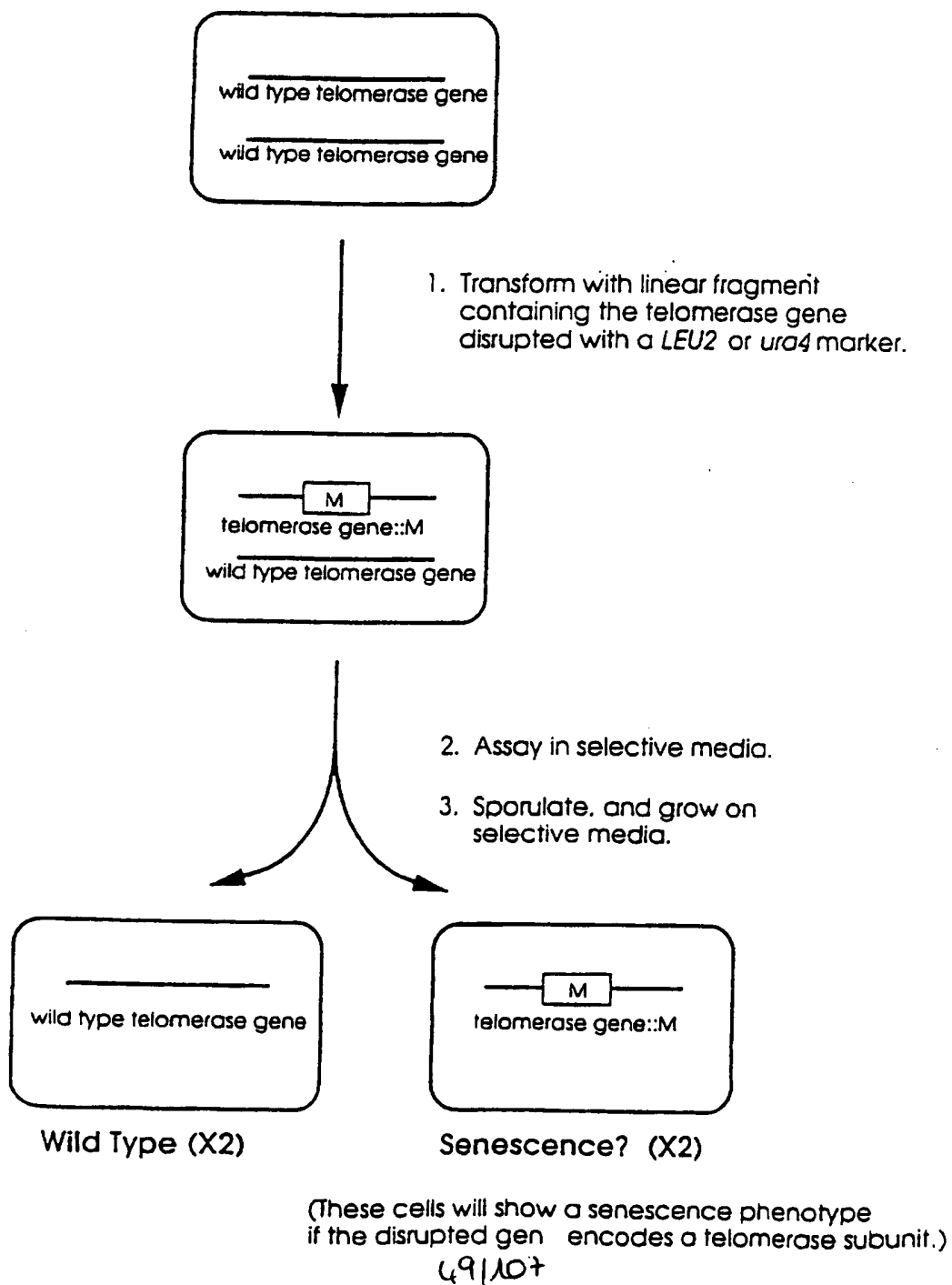


Figure 44

An Example of Confirmation of *lez1* disruption By PCR

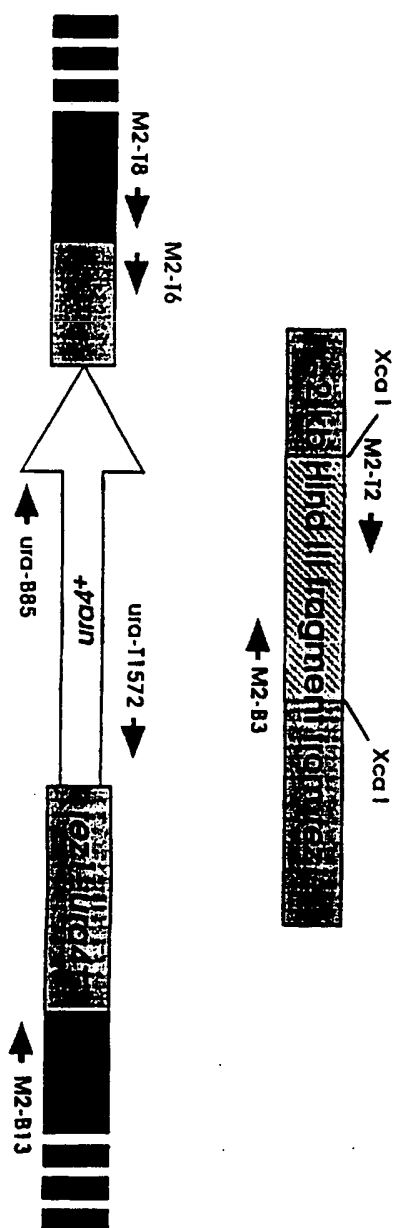
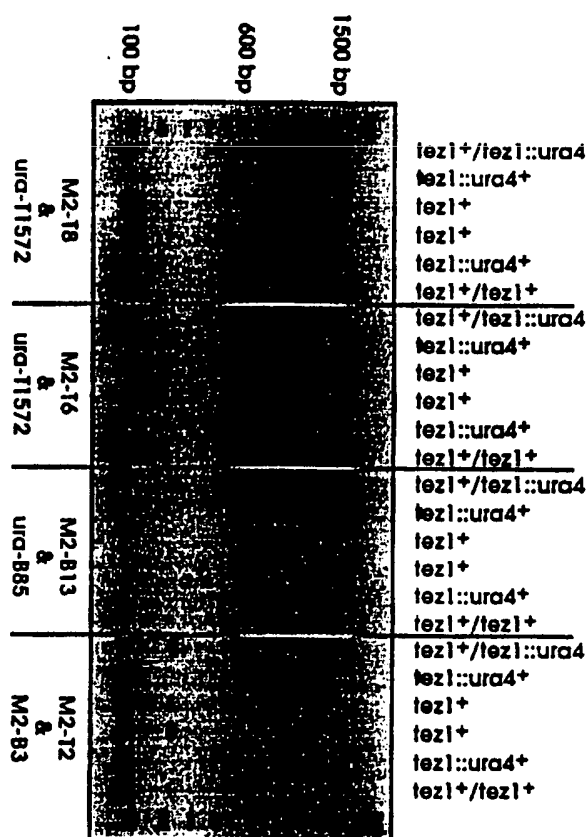


FIGURE 45

*Tez1* disruption causes progressive shortening of telomeres in *S. pombe*

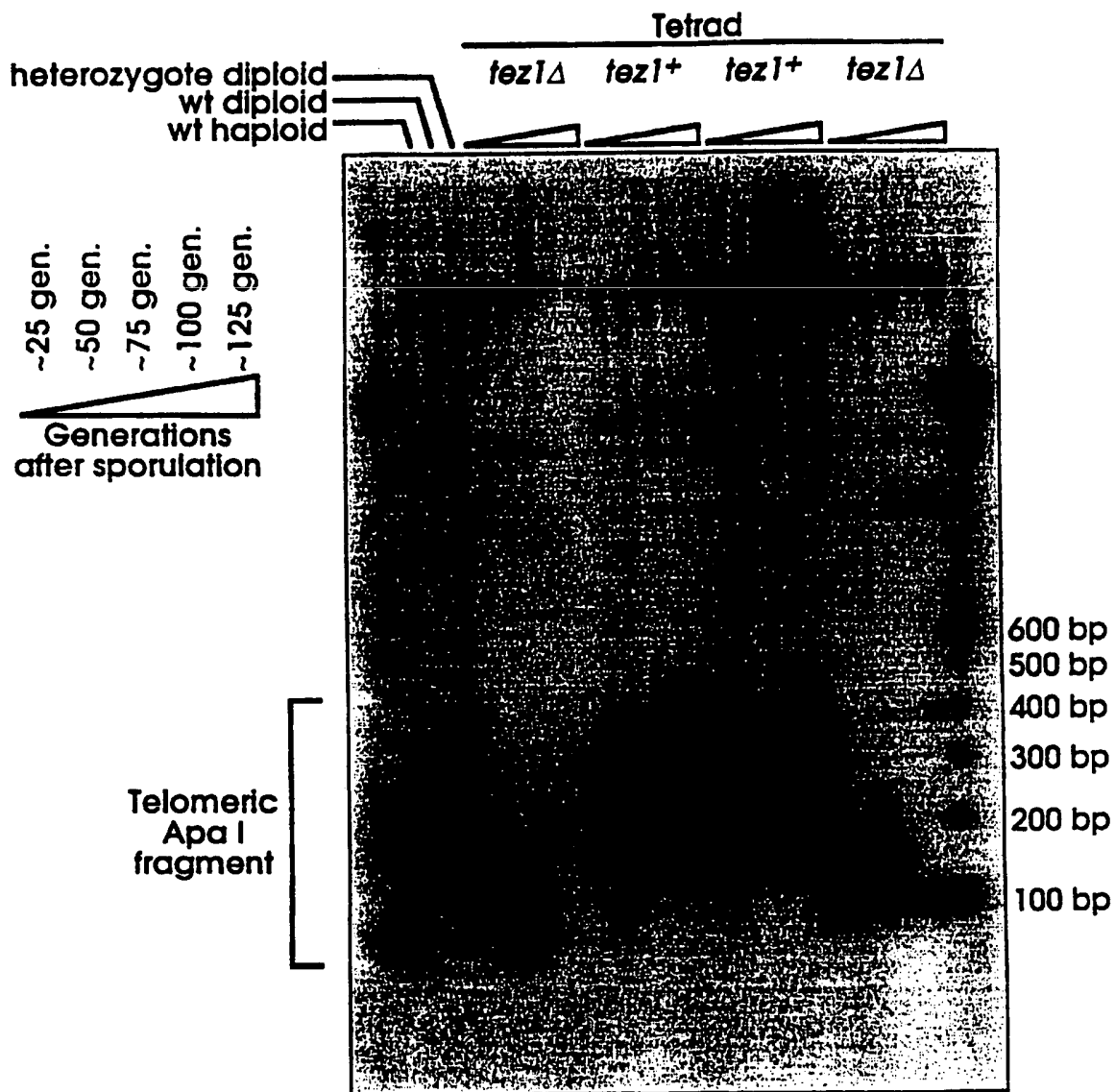


FIGURE 46

1 ggtaccgattttacttttcccttttccataagctaattgcttccctcgaacgctccctaaatctctggaaatatttttacaaga 80  
 81 actcaataacaataccaagtc aaactccaatatgaagggtgttatttagtgatcgataaatattttctattttatcggtcgtta 160  
 161 ccaagtataaggacaaaaagaacaacttcccttccccctaaagacttttacttttactaatttacttttcaaatatatttcg 240  
 241 gggttcgcttactttttaaactcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgctcattggatat 320  
 321 agctcttggagtagcttcacagaaatccttacaatcttctgatgagactatattagattcattacagtcctcgatatttc 400  
 401 ttaacatggagcctttacacttttagatgagtcacgtcgcgtatgaggagtatttggtatcatccaacgcttgccttgaaaag 480  
 481 gttgataatttatitgcaaaatcatgtcctttagtggtggtaatccgcgaaagttttttagtgcttgcacacgtcttagcatg 560  
 561 attgagatattcaaaaaatttctatccactacaactcctttaaagcggttttatttttctattttctatttctcatgttctt 640  
 641 ccaaatatgtatcatctcgtatttaggcttttttccgtttttactcctggaaatcgtacctttttcactattccccctaatga 720  
 721 ataattcaaatattagtttctgcttataattgatagtagtagaaagattgggtgattcttactcgtgtaattgttattagttctaaa 800  
 801 gatacttttgcaaaaacatttattagctaccattatatacaaaaaaaatcctataattataaatatttaaccaatatttgcgggtc 880  
 881 acctattttattttaaacgcttatgattcagtaggacactttgcatatataatagtttatgcttaattggttacttgtaaccttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018  
 1 M T E H H T P K S R I L R F L E N Q Y V 20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078  
 21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138  
 41 Y S N I C E R L R S D V Q T S F S I F L 60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198  
 61 H S T V V G F D S K P D E G V Q F S S P 80

1199	AAA TCC TCA CAG TCA GAG	gtatatacatatcttctgctcttgatctctctctctctctctctcgaggatagctaatatcatcgggcag	1272
81	K C S Q S E		86
1273	CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA		1332
87	L I A N V V K Q M F D E S F E R R R N L		106
1333	CTG ATG AAA GGG TTT TCC ATG	gtaaggtattcttaattgcgaatactttaccttgcaattactgtttcaagaga	1405
107	L M K G F S M		113
1406	tcgtattttaaaccgacaaag	AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469
114		N H E D F R A M H V N G V Q N	128
1470	GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA		1529
129	D L V S T F P N Y L I S I L E S K N W Q		148
1530	CTT TTG TTA GAA AT	gtaaataccgggttaagatgttcgcgacatttgaacaagactgcacaagtatag T ATC GGC	1601
149	L L L E I		I G 155
1602	AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG CCT CTT CCA AAT GAC		1661
156	S D A M H Y L L S K G S I F E A L P N D		175
1662	AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG		1721
176	N Y L Q I S G I P L F K N N V F E E T V		195
1722	TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA		1781
196	S K K R K R T I E T S I T Q N K S A R K		215
1782	GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT		1841
216	E V S W N S I S I S R F S I F Y R S S Y		235
1842	AAG AAG TTT AAG CAA G	gtaactaataaccgttatctctctcataacttaattcttag AT CTA TAT TTT AAC	
1907			
236	K K F K Q D		L Y F N 245
1908	TTA CAC TCT ATT TCT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG		1967
246	L H S I C D R N T V H M W L Q W I F P R		265
1968	CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA		2027
266	Q F G L I N A F Q V K Q L H K V I P L V		285
2028	TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA		2087
286	S Q S T V V P K R L L K V Y P L I E Q T		305
2088	GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT		2147
306	A K R L H R I S L S K V Y N H Y C P Y I		325
2148	GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG		2207
326	D T H D D E K I L S Y S L K P N Q V F A		345
2208	TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA		2267
346	F L R S I L V R V F P K L I W G N Q R I		365
2268	TTT GAG ATA ATA TTA AAA G	gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT	2336
366	F E I I L K D		L E T 375

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FIGURE 46 (cont.)

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396  
 376 F L K L S R Y E S F S L H Y L M S N I K 395

2397 gtaatcatgccaaatttttttaccatttaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465  
 396 I S E I E W L V L G 405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525  
 406 K R S N A K M C L S D F E K R K Q I F A 425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585  
 426 E F I Y W L Y N S F I I P I L Q S F F Y 445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645  
 446 I T E S S D L R N R T V Y F R K D I W K 465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG 2705  
 466 L L C R P F I T S M K M E A F E K I N E 485

2706 gtatttttaagtcatttttttgcaaaaagctaataatttttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775  
 486 N N V R M D T Q K T 495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835  
 496 T L P P A V I R L L P K K N T F R L I T 515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatttaatttttggtcatcaatgtacttttacttttaattctatta 2906  
 516 N L R K R F L I K 524

2907 tttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967  
 525 M G S N K K M L V S T N Q T L R P V 542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027  
 543 A S I L K H L I N E E S S G I P F N L E 562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaac 3088  
 563 V Y M K L L T F K K D L L K H R M F G 581

3089 tatataatgcgcgattcttcattattaatttttcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155  
 582 R K K Y F V R I D I 591

3156 AAA TCC TGT JAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215  
 592 K S C Y D R I K Q D L M F R I V K K K L 611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275  
 612 K D P E F V I R K Y A T I H A T S D R A 631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttttaccatggaaatttttttaacaa 3343  
 632 T K N F V S E A F S Y F 643

3344 atttttttttcag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405  
 644 D M V P F E K V V Q L L S M K T 659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465  
 660 S D T L F V D F V D Y W T K S S S E I F 679

3466 AAA ATG CTC AAG GAA CAT CTC TCT CGA CAC ATT GTT AAG gtataccaattgttgaattgtataaaca 3532  
 680 K M L K E H L S G H I V K 692

FIGURE 46 (cont.)

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593  
 693 I G N S Q Y L Q K V G I P Q G S 708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653  
 709 I L S S F L C H F Y M E D L I D E Y L S 728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713  
 729 F T K K K G S V L L R V V D D F L F I T 748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattccc 3777  
 749 V N K K D A K K F L N L S L R G 764

3778 taagtcttaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840  
 765 F E K H N F S T S L E K T V 778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900  
 779 I N F E N S N G I I N N T F F N E S K K 798

3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960  
 799 R M P F F G F S V N M R S L D T L L A C 818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020  
 819 P K I D E A L F N S T S V E L T K H M G 838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataaccag A TCG 4089  
 839 K S F F Y K I L R S 848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149  
 849 S L A S F A Q V F I D I T H N S K F N S 868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209  
 869 C C N I Y R L G Y S M C M R A Q A Y L K 888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtactttactttaactaga 4274  
 889 R M K D I F I P Q R M F I T D 903

4275 aaagtcattaacttaacccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339  
 904 L L N V I G R K I W K K L A 917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtcc 4401  
 918 E I L G Y T S R R F L S S A E V K W 935

4402 ggtcttcgagacttcagcaatattgacacattcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468  
 936 L F C L G M R D G L K 946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528  
 947 P S F K Y H P C F E Q L I Y Q F Q S L T 966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA 4588  
 967 D L I K P L R P V L R Q V L F L H R R I 986

4589 GCT GAT TAA tgtcattttcaatttattacatacatccttttactactgtgtcttaacaataaccattactaagata 4665  
 987 A D 989



FIGURE 46 (cont.)

4666 gctgacccccaaagcaagcactactataggatttcttagtaaaagtaaaattaatctcgcttattagcttttgattgacttgtct 4745  
4746 ttatcccttatacttttaagaagattgacagtggttgctgactactgcccacatgcccactaaacgggagtggttaaaca 4825  
4826 ttaaaagtaatacatgaggctaactctcccttccatttagaataaggaaagtggctttctataatgaataatgcccgcacta 4905  
4906 atgcaaaaagacgaagattatcttctaaacaagggggattaaagcatatccgaaggaaaagagagcaatatacccagtgct 4985  
4986 gctgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattcttggtgaccgaatcttggtaaaagc 5065  
5066 cccagggttatccatgggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaaatagcttcattta 5145  
5146 atgtctttatacaagggttttgttttttccctgacttcaattcttgcatgggtgaaaagaaatagctgttaagccattattgga 5225  
5226 tccgaaatagccaaattcttctgggttctctcaaagcgggaagctctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305  
5306 tcctgattttaaaggagggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagccctaatttttgc 5385  
5386 aaaaaagaaaaatcatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatcccttgatgtcaata 5465  
5466 acttctatcttctgaaatgcatggctctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc 5544

FIGURE 47

```

      1
GCCAAGTTCCTGCACTGGCTG  met ser val tyr val val glu leu leu
                        ATG AGT GTG TAC GTC GTC GAG CTG CTC

10      20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

      30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

40      50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

      60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

70      80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

      90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACC TTC CGC AGA

100      110
glu lys ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

      120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130      140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

      150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160      170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

      180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

```

FIGURE 47 (cont.)

```

190                                     200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

                                     210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220                                     230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

                                     240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250                                     260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

                                     270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280                                     290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CCG AAG ACA

                                     300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310                                     320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

                                     330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340                                     350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

                                     360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370                                     380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

```

FIGURE 47 (cont.)

390  
 leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln  
 CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG  
 400 410  
 ala tyr arg phe his ala cys val leu gln leu pro phe his gln  
 GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG  
 420  
 gln val trp lys asn pro his phe ser cys ala ser ser leu thr  
 CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA  
 430 440  
 arg leu pro leu leu leu his pro glu ser gln glu arg arg asp  
 CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT  
 450  
 val ala gly gly gln gly arg arg arg pro ser ala leu arg gly  
 GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC  
 460 470  
 arg ala val ala val pro pro ser ile pro ala gln ala asp ser  
 CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG  
 480  
 thr pro cys his leu arg ala thr pro gly val thr gln asp ser  
 ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC  
 490 500  
 pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys  
 CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC  
 510  
 pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp  
 CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC  
 520 530  
 his pro gly leu met ala thr arg pro gln pro gly arg glu gln  
 CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG  
 540  
 thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly  
 ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG  
 550 560  
 arg gly gly pro his pro gly leu his arg trp glu ser glu ala  
 AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC  
 564  
 OP  
 TGA GTGAGTGTTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC  
 CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

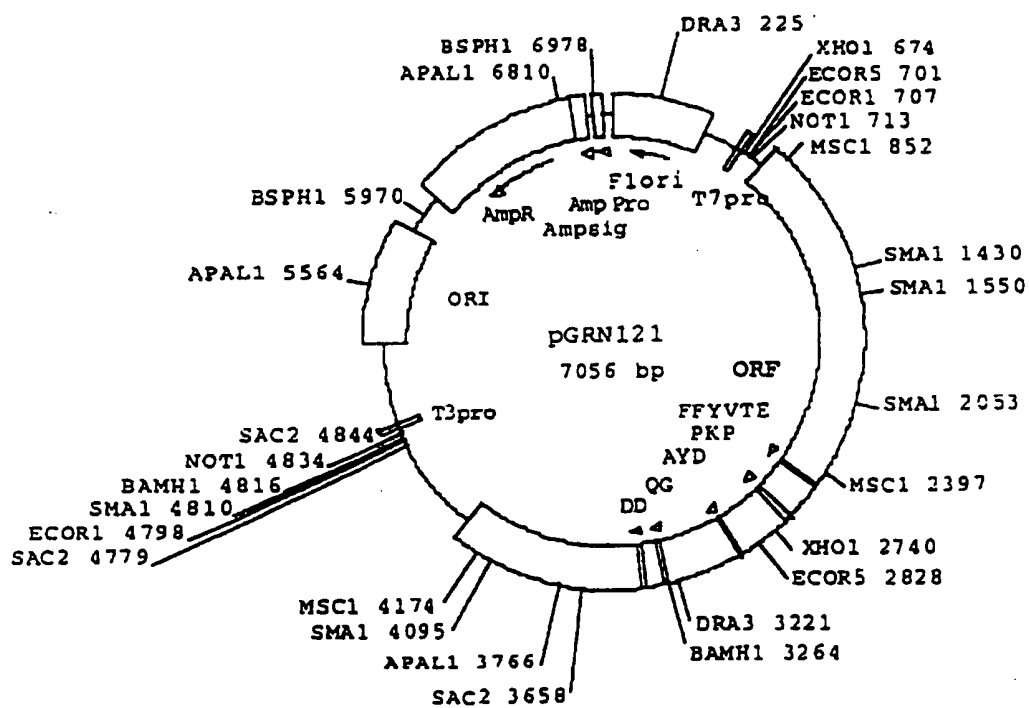
## FIGURE 47 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT  
CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTACCCCTTCGCCCTGCCTTCC  
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG  
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG  
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT  
TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 48

Motif -1	
Ep p123	...LVVSLIRCFFYVTEQQKSYSKT...
Sp Tez1	...FIIPILQSFFYITESSDLRNRT...
Sc Est2	...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1	...YVVELLRSFFYVTETTFQKNRL...
consensus	FFY TE
Motif 0	K
	p hhh K hR h R
Ep p123	...KSLGFAPGKLRLLIPKKT--TFRPIMTFNKKIV...
Sp Tez1	...QKTTLPPAVIRLLPKKN--TFRLLITNLRKRFL...
Sc Est2	...TLNFNHSMRIIPKKSNNFRIIAIPCRGAD...
Hs TCP1	...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus	R PK RI
Motif A	AF
	h hDh GY h
Ep p123	...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1	...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2	...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1	...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
consensus	F D YD
Motif B	hPQG pShh
Ep p123	...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1	...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2	...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1	...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus	G QG S
Motif C	Y
	h F DDhhh
Ep p123	...PNVNLLMRLTDDYLLITTQENN...
Sp Tez1	...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2	...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1	...RRDGLLLRLVDDFLLVTPHLTH...
consensus	DD L
Motif D	Gh h cK
Ep p123	...NVSRENGFKFNMKKL...
Sp Tez1	...LNLSLRGFEEKHNFST...
Sc Est2	...KKLAMGGFQKYNKA...
Hs TCP1	...LRTLVRGVPEYGCVV...
consensus	G

FIGURE 49



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FIGURE 50

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC  
51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC  
101 AGCCACTACC GCGAGGTGCT GCGGCTGGCC ACGTTCGTGC GCGCCTGGG  
151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCGGC  
201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC  
251 CCGCGCGCCC CTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC  
301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT  
351 TCGGCTTCGC GCTGCTGGAC GGGGCCCCG GGGGCCCCC CGAGGCCTTC  
401 ACCACCAGCG TGCAGCTA CCTGCCAAC ACGGTGACCG ACGCACTGCG  
451 GGGGAGCGGG GCGTGGGGG TGCTGCTGCG CCGCGTGGG GACGACGTGC  
501 TGGTTCACCT GCTGGCACGC TGCGCGTNT TTGTGCTGGT GGNTCCAGC  
551 TGCGCCTACC ANGTGTGCGG GCGCGCGCTG TACCAGCTCG GCGCTGCNAC  
601 TCAGGCCCCG CCCCCGCCAC ACGTANTGG ACCCGAANGC GTCTGGGATC  
651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG  
701 CCAGCCCCG GTGCGAGGAG GCGCGGGGG AGTGCCAGCC GAAGTCTGCC  
751 GTTGCCCAAG AGGCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC  
801 CCGTTGGGCA GGGGTCTGG GCCACCCCG GCAGGACGCC TGGACCGAGT  
851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC  
901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCAC CCATCCGTGG  
951 GCGGCCAGCA CCACGCGGG CCCCCATCCA CATCGCGGCC ACCACGTCT  
1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCTCTAC  
1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCTACTC AATATATCTG  
1101 AGGCCCAGCC TGAATGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG  
1151 TTCCAGGCCT TGGATGCCAG GATCCCCCG AGGTTGCCCC GCCTGCCCA  
1201 GCGNTACTGG CAAATGCGG CCGTGTCTT GGAGCTGCTT GGAACACG  
1251 CGCAGTGCCC CTACGGGGTG TTCTCAAGA CGCACTGCCC GCTGCGAGCT  
1301 GCGGTACCC CAGCAGCCG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC  
1351 TGTGGCGGCC CCCGAGGAG AGGAACACAG ACCCCGTCG CCTGGTGAG  
1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGGGGC  
1451 CTGCCTGCGC CGGCTGGTGC CCCAGGCCT CTGGGGCTCC AGGCACAACG  
1501 AACGCGCTT CTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT  
1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TCGGGACTG  
1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGAGAGC  
1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT  
1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTC TTTTATGTCA CGGAGACCAC  
1751 GTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT  
1801 TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG  
1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT  
1901 GACGTCCAGA CTCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG  
1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGAG AGAAAAGAGG  
2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG TGCTCAACTA  
2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCTGG  
2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG  
2151 GACCCGCGCG CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA  
2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA  
2251 AACCCAGAA CACGACTGCG GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC



FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC  
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA  
2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG  
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC  
2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG  
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG  
2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGCCTTGGT  
2651 GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC  
2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG  
2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC  
2801 GGCTTTTGTT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TCGGCCTGC  
2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC  
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGTGG  
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTACA  
3001 GCCTGTTTCT GGATTTCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC  
3051 ATCTACAAGA TCCTCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT  
3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCCCA TTTTCTGCTC  
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG  
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC  
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC  
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCAG  
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC  
3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT  
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC  
3501 GCCGGGCTCT ACGTCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC  
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT  
3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA  
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG  
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA  
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC  
3801 GCCCTGCCCT CTTTGCCTT CCACCCCAAC CATCCAGGTG GAGACCCTGA  
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG  
3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT  
3951 GGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT  
4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIGURE 51

```

GCAGGCTTGTCTCTATCTGCGACGTGGAAGGCGCTTGGCCGCTACCCCGGGAATCC
1 ----- 60
GTTGCGGACGCGAGGACGAGGCTGACCCCTTGGGACCGGACCGGCTGGGGCGCTACGG

A A I R P A A H V G S P C P G H P K D A -
B Q K C V L L R T W E A L A P A T P A M P -
C S A A S C C A R G K P W F R P P F R C R -

CCCGGCTCCCGCTCCGAGCGGCTGCGCTGCTGCTGCGCAACCACTACCGGAGTATCT
61 ----- 120
CCGCGAGAGGCGGAGGCTGCTGCGGAGGAGCGAGCGGCTGGTGATGGCGCTCCAGGA

A R S P L F E R A L P A A Q P L P E G A -
B F A P K C R A V H S L L K E H Y R E V L -
C A L P A A E P C A P C C A A T T A R C C -

CCCGCTGCGCGCTTCTGTCGCGGCTGCGGACCGAGGCTGCGCGCTGCTGCGAGCGG
121 ----- 180
CCGCGACGCTGCGAGGACCGCTGCGACCGCTGCGGCTGCGGACCGCGGACCGCTGCGG

A A G H V R A A P G A P G I A A G A A R -
B F L A T F V R R L G P Q G W R L V Q R G -
C R W P R S C G A W G P R A G G W C S A G -

GCACCGCGCGCTTTGCGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGG
181 ----- 240
CCTGCGCGCGGCGGAGGCGGCGGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGG

G P G G F P R ? G Q P ? ? G V R A L G ? -
B D P A A P R A ? V A ? C ? V C V P W ? ? -
C T E R L S A R W W P ? A W C A C T G ? ? -

AAGAGGCGGCGGCGGCGGCTTCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGG
241 ----- 300
TTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGG

? A A P R R P L L P P C V L P E ? ? G G -
B ? ? P P A A P S P R Q V S C L ? ? L V A -
C G ? P P ? P P P S A R C P A ? ? ? W W P -

CCGAGTCTGCGGAGGCTTCTGCGGCGGCGGCGGCGGCTTCTGCGGCGGCTTCTGCGG
301 ----- 360
GGCTGCGGCGGCTTCTGCGGCGGCGGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGG

P S A A ? A V R ? R R E ? R A G L E L R -
B P V L ? ? L C ? R G A ? N V L A P Q P A -
C E C C ? ? C A ? A A R ? T C W P S A S R -

GTTCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGG
361 ----- 420
CGAGGAGCTTCTGCGGCGGCGGCGGCGGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGG

A A C R G P R G P P R G L H H Q R A Q L -
B L L G G A R G G G P P E A F T T S V R S Y
C C W T G P A G A P P R P S P P A C A A F -

```

**FIGURE 51 (cont.)**

OTGCCCAAGGCTACCGAAGCATTCCGAGAGGATGGTGTGGGTGGTGTTGCTGGT  
421 ----- 490  
GCACGGGTTGTACCACTGTCCTGCTGACGGGCTCTCTGCTCCGTCAGCCCTGCAAGACACUC

P A Q H G D R R T A G E P G V G A A A A  
L P N T V T D A I R G S C A W G L L L K -  
C P T R \* F T K C C G A G R G G C C C A -

CCCCGTGGGGAACGAGCTGCTGTTCACCTCTCTGGGAACTXDXLYNTMTTCTCTGTT  
491 ----- 540  
GCGCCAGCCCGCTCTCTACGAGCAAGTGGACGACCGCTCCGACCGCCNANAAACAGACCA

P R C R R R A G S P A G T L R ? ? C A G -  
K V G D D V L V H L L A R C A ? F V L V -  
A W A T T C W F T C W H A A R ? L C W W -

GNNITCCAAGCTGGGCTAACNGTGTGGGAGCCCGGCTGTACCAAGTGGGCTGGCAC  
541 ----- 600  
CCNAAGGTGAGACGCGATGCTTCACACGCCCCCGGCGACATGCTCCACCTCCGACGCTC

G S Q L R L P ? V R A A A V P A R R C ? -  
Y P S C A Y ? V C G P P L Y G L G A A T -  
P F A A P T ? C A G R R C T S S A L T L -

TCAAQTCGCGCCCCCGGCACAGCTANTGCACCCCAAGGCTCTGCGATCCAAAGCGCT  
601 ----- 650  
AGTCTGGGCGGCGGCGGCTGTGGCATTAAGCTGAGCTTNCCASAGCTTAGATTTCGCGTA

S C P A P A T R ? M T R ? R L G S N G P -  
Q A R P P P H A ? G P E ? V W D P T G L -  
R P G P R H T L ? D C ? A S G I Q E A W -

GRAGCATAGCGCTCAAGGAGGCGCGCTCCCGCTCGGCTGCCAGCCCGCGGCTGACAGAG  
661 ----- 720  
CCTTRATATACAGTGTCTCGGCGCGAGGGACCGGACCGCTCGGCGCGACAGCTGCTC

G T I A S C R P C S P W A A S P G C E E -  
E P \* R G G G R C P P C L P A P G A R R -  
N H S V R E A G V P L G C Q P R V R G G -

CGGCGGCGGCAATGCGAGCGGAGGCTTCCGCTTCCCAAGAAGCGGCGGCTGCTGCTG  
721 ----- 780  
CGGCGCGCGCTCACAGTTCGATTACAGAGGCAAGGATTTCTGCGGCTGCGACAGCGAGG

A R Q Q C O P K S A V A Q E A Q A W K C -  
H G C S A S R S L P L P K R P R R G A A -  
A G A V F A E V C R C F R G P G V A L ? -

CCTTACGCGTACAGAGCGCGCTTGTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
781 ----- 840  
GCGACTGCGCTGCTGCTGCGGCAACCGTCCCGCAGGACCGGCTGCGGCTGCTGCTGCTGCT

P \* A C A D A K W A G V L G P P G Q D A -  
P E R T P V G Q G S W A H P C R T F -  
L E R S G R P L G R C P G P T R A C E L -

FIGURE 51 (cont.)

```

      TGGAGGAGTGAAGGCTGCTTTCTGTGTGTGTGACCTGCCAGACCCCTGCAAGAGAGCCAC
841 ----- 900
      AACCTGCTCACTGACACCAAGACACACACAGTGGACCGCTCTGGGCGGCTTCTTTGGGTC
      W T E * P W F L C G V T C Q T R R R S H -
      G P S D R G F C V V S P A R F A E E A T
      D P V T V V S V W C H L P D P F K K P F -
      CTCTTGGAGAGTGGCTCTCTGTGGACGGCGGCACTGCCACCGATGCTGGGGCTGGACCA
901 ----- 960
      CACAAAGCTGCCACCGGAGAGACCGTGTCTGTGTGAGGCTGGGTAGGCACCCGCGGCTCGT
      L F C G C A L W H A F L F P T R G F F A
      S L E G A L S C T R H S H P S V Q R Q H -
      L W K V R S L A R A T P T H P W A A S T -
      CCAGTGGAGGCTGGGATTCACATGCGCGCCACCACTGCTGGGACACCTTCTTCTCTCTCT
961 ----- 1020
      GCTGACCGCTGGGCTGTAGGTGTAGCGCGGCTGTGTGACGACCTGTGCGGAGCAAGAGGCG
      P R C P P I H I A A T T S W D T F C P P -
      H A G P P S T S R P P R P G T R L V P P
      T R A F H P H R G H H V L G H A L S P C -
      GTGTAGGCGGAGAGCAAGCACTTCTCTACTCTCTCAGGCGACAGNACACTGCGGCGCTTC
1021 ----- 1080
      CACATGGCGCTCTGTATTGTGTGAGGAGATGAGGAGTCCGCTGTTCTGTCAGGCTGAGG
      V Y A E T K H F L Y S S C D K ? T A ? L -
      C T P R P S T S S T P Q A T ? T L R P S -
      V R K D Q A L F L L L R R Q ? H C ? P P -
      CTTCTATCTCATATATCTGAGCGCCAGCGCTTACTGCGGCTCGAGGATTTGCTGAGAGC
1081 ----- 1140
      GAAGATGAGCTTATATAGACTTCGCGCTCTGACTGACCGCAAGCTTCCAAAGACCTCTTGT
      L P T Q Y I * G P A * L A F G R F V E T
      F L L N I S E A Q P D W R S C G S W R Y -
      S Y S I Y L R P S L T G V R E V R G D ? -
      NTCTTCTGCTTCCAGCGCTTGGATGCAAGATTCCCGGCAAGTTGCGCGGCTTGGCGCA
1141 ----- 1200
      NAGAPAGGCAAGCTTCTGAACTTAACTTCTTAAAGCGGCTTCTTAAAGCGGCTTAAAGCG
      P F L V P G L G C Q D S P Q V A P P A P -
      G F W F Q A L D A R I P R R L P R L P Q -
      L S G S R P W H P G F P A G C P A C F S -
      GCGNTACTGCAATGCGCGCGCTGTTCTGTGAGCTTCTTGGAGGACAGCGCGCTGCTCT
1201 ----- 1260
      GCGNATGAGCGTTTACGCGCGGCAAGAGCTTCTGAGGAGAGCTTCTGCGGCTTCAAGG
      A * L A H A A P V S G A A W E P R A V F -
      R Y W Q H R F L F L E L L G N H A Q C F -
      P T G K C G P C F W S C L G T T K S A F -

```

FIGURE 51 (cont.)

```

CTAGGGGTTTCTTCTCAAGACCGACTGCCCGCTGCCGAGTGGGGTACCCCAAGAGGCGG
1261 ----- 1320
CATGACCCACAAAGGATTCTGTGTGAGGAGGACCGCTGAGCCCACTGGGGTGGTGGG
L R G V P Q U A L P A A S C G H F S S R -
D Y G V F L K T H C P L R A A V T P A A G -
C T G C S S R R T A R C E L R S P Q Q P V -

TGTCTGTGCGCGGAGAAACCCCAAGGCTCTGTGGCGGCCCTGAGGAAGAGAACACAG
1321 ----- 1380
ACAGACACCGGCGCTCTTGGGGTCCCGAGACACCGCGCGGGGCTCTCTCTCTTGTGTC
C L C P G E A P G I C G G P R G G G T Q -
D V C A H E K P Q G S V A A P E E E E H R -
C G V P G R S P R A L W R P P R R E N T D -

ACCGCGGTGGCTGTGTGACCTGTCCCGCAGCAGCAGAGTGTGCAAGTGTAGCGCT
1381 ----- 1440
TGGGCGACCGGACACAGTTCAGGAGGGGCTGTGTGTGTGCGAGAGTTCACATGCGGA
T F V A W C S C S A S T A A P G R C T A -
D P P S P G A A A P P A Q Q P L A G V R L -
C P R R L V Q L L R Q H S E P W Q V Y G F -

TGTGTGGGGCTGCTGTGCGCGCTGTGTGCGCGCGGCTCTGTGTGTGCAAGTGTAGAG
1441 ----- 1500
AGCAGGTGTGAGAGGAGGAGGCGGAGCGGAGTGTGCGAGAGGCGGAGTGTGCGAG
S C G P A C A G W C P Q A S G A F G T T -
D H A G L P A P A G A P H P L G L Q A Q R -
C V R A C L R R L V P P C L W G S E H N E -

AAGCGGTTTCTTCAAGGACCAAGAGTTCATCTCCCTGGGGAAGCATGCGAGTCT
1501 ----- 1560
TTGCGGGAAGGAGTCTGTGTGCTTCTTCAACTAGAGGAGGCGGCTTCTGACGTTGAGA
N A A S S G T P R S S S P W G S H P S S -
D T P L P Q E H Q E V H L P G E A C Q A L -
C P R F L R N T K K Y I S L G K H A E L S -

GCTGTGAGGAGCTGAGTGTGAGAGTGAAGCTGCGCGGCTGCGCTTGTGCTGCGAGGCT
1561 ----- 1620
GCGAAGTCTTCACTGACCTTCTATCTGCAAGCTGTGAGCGAGAGGAGTGTGCTGAG
R C R S * R G R * A C G T A L C C A G A -
D A A G A D V E D E R A G L R L A A Q E P -
C L Q E L T W K H S V R D C A W L R R S P -

CAAGGTTTCTGCTTCCCGCGCAGAGACCGCTCTGCTTGAAGATCTGCGAGAGT
1621 ----- 1680
GTCCCGACCGACACAGGCGCGGCTGTGTGTGCGAGAGGCTCTCTTGAAGAGGTTCA
Q Q L A V F R P Q S T V C V R R S W F S -
D R G H L C S C R R A T S A T G D P G Q V -
C G V G C V P A A E H R L R E E I L A K F

```

FIGURE 51 (cont.)

TCTCTACTGCTCCATCACTGTGTACCTGCTGAGCTCTTCAGGCTCTTCTTTTATATCA  
 1691 ..... 1740  
 AGGAAGTGAAGCACTACTTACACATCCAGCAGCTTCCAGAGTCCAGAAACAAAATACAGT  
 A C T G \* V C T S S S C S C L S F H S -  
 B P A L A D E C V K R R A A Q V F L L C H -  
 C L H W L H S V Y V V E L L R S F F Y V T -  
 CCGAGACCACTTTTCAAAAGACAGGCTCTTTTCTTACCGGAAGAGTGTCTGAGCAAGT  
 1741 ..... 1800  
 GCCTCTGGTCCAAATTTTCTTCTCCAGACAAAAGATCCCTTCTCAGAGCTCCTTCA  
 A R P S E K R T G S F S T G R V S G A S -  
 B G D H V C K E Q A L F L P E E C L E Q V -  
 C E T T F Q K N R L F F Y R K S V W Y K L -  
 TTCAAAGCATTTGAATCAGACACACTTGAAGAGGGTCCAGCTTCCGGAGCTTCTGFAAG  
 1801 ..... 1860  
 AGCTTTCTTAAGCTAGTCTGTCTGAACTTCTCCCAAGTCCAGCCCTTACAGCCTTC  
 C K A L E S D S T \* K G C S C G S C R K -  
 B A K H W N Q T A L E E C A A A C A V C S -  
 C Q S T G T R Q H L K R V Q L R E L S E A -  
 CAGAGTTCAGTCAACATCCGAGCCAGCCGCCCTCTCTCAGCTCCAGACTTCTCTTCA  
 1861 ..... 1920  
 GTCTCCAGTCCCTCTGTAGCCCTTCTGCTCCGCGCCAGCTCCAGCTTCAAGTCAAGT  
 Q R E G S I G K P G P P C \* R F D S A S -  
 B K G Q A A S C S Q A R P A D V O T F L H -  
 C E V S Q H R E A R P A L L T S R L K F I -  
 TCTCCAGCTTCAAGGCTCCGCGGATTTGTACATGGACTAGCTGTCTGGAGCCAGAA  
 1921 ..... 1980  
 AGGAGTTCAGACTTCCGAGCCGCCCTTACACTTCTTCTGATCCAGACCTCTGCTTT  
 S P E L T G C G K L \* T W T T S W E P E -  
 B P Q A \* S A A A D C E H C L R R G S Q H -  
 C F K P D G L R P I V N M D Y V V G A K T -  
 CTTTCTCCAGACAAACAGCCGCCGCTCTCAGCTCCAGGCTTCAAGTCACTTCTCAAGS  
 1981 ..... 2040  
 CCAAGCTTCTTTTCTTCTCCGCGCTCCAGAGTCCAGCTCCAGCTTCTTCAAGTTCGCT  
 R S A E K R G P S V S P H G \* R H C S A -  
 B V P Q R K E G R A S H L E G E C T V Q R -  
 C F R E K R A E R L T S R V K A L F S V -  
 TCTCTACTAGCAAGCCGCGCGCTCTCTCCGCGCTTCTTCTTCAAGTCTG  
 2041 ..... 2100  
 AGGAGTTCAGACTTCCGAGCCGCCCTTACACTTCTTCTGATCCAGACCTCTGCTTT  
 C E T T S G R G A P A S W A P L C W A W -  
 B A Q L R A G A A P K P C G R L C A G P G -  
 C L N Y E E A R R P G L L G A S V L G L D -

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[illegible]

FIGURE 51 (cont.)

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2521  CTTATCTCACTTCCACGCGGATCCGCGAAGGCTCTATCTCTCTGCTCTGCTCTGACCC
----- 2590
2522  GATATCACTTACGCTCCCTTAGGCGCTTCGCGAATTAGGAGGCTGCGACGACCTGG
-----
A   P T S S A R G S R R A P S S P S C S A A -
D   L A P V P G D P A G L H P L H A A L Q P -
C   Y V Q C C C I P Q S I L S T L L C S L -

2581  TTTATTAAGGTCACATGAGAGCAAGCTTTTTCGCGGATTCGCGGAGGCTTCTCTC
----- 2640
2582  ACAAGATTCGCTTATACCTCTTCTTCGACAAACGCGCTTACGCGCGCTGCGCGACGAG
-----
A   C A T A T W K T S C L R C F G G T C C S -
D   V L R R H G E Q A V C G D S A G R A A P -
C   C Y G D H R N K L F A G I R E D G L L L -

2641  TCGCTTTCTGCAATCTTCTTCTTCTGTCACAGCTCAGCTCAGCGAGCGAAAACTTCC
----- 2700
2642  AATCAAACTCCTTCTAAGAGACAACTCTCTGAGCTTCTGAGCTCTCTCTCTTCTGAGG
-----
A   C V W W H I S C W * H L T S P T K K P S -
D   A P G G * F I V G D T S C H T R E N L P -
C   R L V D D F L L V T P H L T H A K T F L -

2701  TCAGGAGCTCTCTCCAGCTCTCCCTCACTATGCGCTGCTCTGTAACCTTGGGTAAGACAG
----- 2760
2702  AGTCTTGGGACCGGCTTCACAGGAGCTCTAAGCTTCAAGGAGGCTTCAAGGCTTCTCTC
-----
A   S G F W S E V S L S M A A W * T C G P Q -
D   Q D P G P R C P * V W I R G E L A E D S -
C   F T L V R G V P E Y G C V V N L R K T V -

2761  TCGTCACTTCTCTTGTAGAAGAGAGCGCGCTGCGTGGCAGGCTTTTCTTCAAGTGGCG
----- 2820
2762  AACCACTTGAAGGACATCTTCTCTCTCCAGGAGCGAGCTTCCGAAAGAGCTTACGCGTC
-----
A   W * T S L * K T R P W V A K L L F R C H -
D   G E L P C R R R C P C W H C F C S D A G -
C   V N F P V E D E A L G G T A F V Q M P A -

2821  CCCAGGCTCTATTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
----- 2880
2822  GCGTTCGCGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
-----
A   P T A Y S P G A A C C W I P C P W R C R -
D   P E P I P L V R P A A G Y P D P G G A E -
C   H G L P P W C G L L L L C T R T L E V Q S -

2881  GCGACTACTTCAATATATGCGCGACCTTCATCAGAGCGAGCTTCAAGCTTCAAGGCGG
----- 2940
2882  CGCTTATGAGGTCATATAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
-----
A   A T T P A M P G P P S E P V S P S T A A -
D   R L L Q L C F D L H Q S Q S H L Q P R L -
C   D V S S Y A R T S I R A S L T F N R G F -

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[illegible]

[illegible]

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3781 1100GCAATTGTCAAGGCTGTGAGCTTGGCTTTTGCTTCCAGCCGACGACGAGTTC
----- 3949
AAGCGTTATACAGTGTGCGGACGCGGCAAGCGACGCAACGGAAGGTGCGGTGTGTGCTGCTGAC
F A I V H P S P C P P L P S T P T I Q V -
S S L F T P R P A L L C L P P P P S R W -
P H C S P L A L P S F A F H P H H P G G -
GAGAGCTGTCAAAATACCGCTGTGAGCTGTGGAATTGAGAGTTAGCGAAGGTGTGCGCTTC
3941 ----- 3999
CTCTAGAGACTCTTCTCTGGAGGCTTCGACAGCTTTAAAGCTCACTGTGTTTTCGCGAGCGGAC
S T L K S T L G A L G T W S G Q R V A L -
K P * E G P H E L W E F G V T A G V P L *
D S E E D F G S S C N L E * P K V C P V -
TACACAAGGTAGGAGGCTCGACCTTCGATGAGGATGCTGTGATTCAAATTGAGAGAGAT
3991 ----- 3999
ATGTGTCCGCTCTCTGGAGCTTCGAGCTTACCCCGAGGACAGCCGAGTTTAAAGCTCTCTGCA
Y T G E D P A P G W G S L W V K L G G G -
T O A K T L H L D G G P C G S N W G E V -
H R R C P C T W H C V P V G Q I G G K C
GCTGTGAGAGTAAATCTGAATATATGAGTTTTCATTTTCAAAAAAAAAAAAAAAAAA
3991 ----- 4029
CGACAGCTCATTTTATGACTTATATACTCAAAAAGTCAAAA.TTTTTTTTTTTTTTTTTT
A V G V K Y * I Y E F F S P E K K K K K
L W E * H T E Y N S P S V L K K K K K
C G S K T L N I * V P Q F * K K K K K K -
AAAAAAA
4021 ----- 4029
TTTTTTTT
K K K -
K K -
K K -

```

FIGURE 52

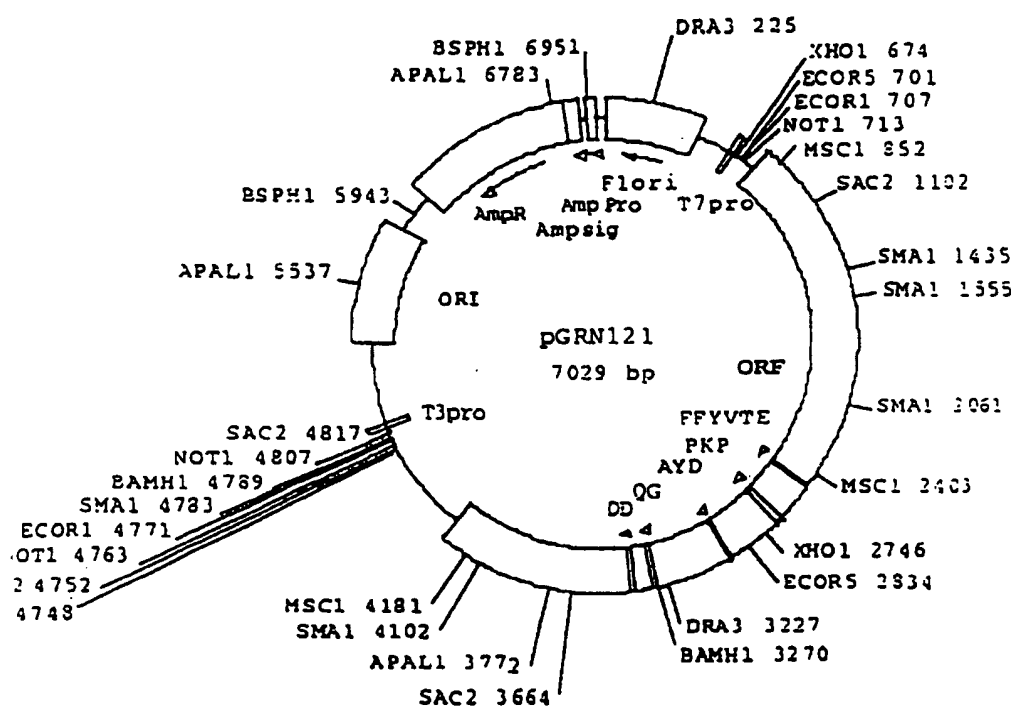


FIGURE 53

```

                                                    1
                                                    met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGCCACCCCCGCG ATG

                                                    10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

                                                    20
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

                                                    30
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

                                                    40
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

                                                    50
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

                                                    60
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

                                                    70
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

                                                    80
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

                                                    90
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

```

FIGURE 53 (cont.)

	140		150											
trp	gly	leu	leu	leu	arg	arg	val	gly	asp	asp	val	leu	val	his
TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	GAC	GAC	GTG	CTG	GTT	CAC
								150						
leu	leu	ala	arg	cys	ala	leu	phe	val	leu	val	ala	pro	ser	cys
CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	GTG	GCT	CCC	AGC	TGC
	170		180											
ala	tyr	gln	val	cys	gly	pro	pro	leu	tyr	gln	leu	gly	ala	ala
GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	CTC	GGC	GCT	GCC
								190						
thr	gln	ala	arg	pro	pro	pro	his	ala	ser	gly	pro	arg	arg	arg
ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	ACT	GGA	CCC	CGA	AGG	CGT
	200		210											
leu	gly	cys	glu	arg	ala	trp	asn	his	ser	val	arg	glu	ala	gly
CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	GCC	GGG
								220						
val	pro	leu	gly	leu	pro	ala	pro	gly	ala	arg	arg	arg	gly	gly
GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	GGC
	230		240											
ser	ala	ser	arg	ser	leu	pro	leu	pro	lys	arg	pro	arg	arg	gly
AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC
								250						
ala	ala	pro	glu	pro	glu	arg	thr	pro	val	gly	gln	gly	ser	trp
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG
	260		270											
ala	his	pro	gly	arg	thr	arg	gly	pro	ser	asp	arg	gly	phe	cys
GCC	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT
								280						
val	val	ser	pro	ala	arg	pro	ala	glu	glu	ala	thr	ser	leu	glu
GTG	GTG	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG

FIGURE 53 (cont.)

290 300  
 gly ala leu ser gly thr arg his ser his pro ser val gly arg  
 GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310  
 gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
 CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330  
 trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
 TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340  
 leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
 CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360  
 leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
 CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370  
 glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
 GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390  
 arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
 CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400  
 leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
 CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420  
 val leu leu lys thr his cys pro leu arg ala ala val thr pro  
 GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430  
 ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
 GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GCC TCT GTG GCG

440														450	
ala	pro	glu	glu	glu	asp	thr	asp	pro	arg	arg	leu	val	gln	leu	
GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	CAG	CTG	
460															
leu	arg	gln	his	ser	ser	pro	trp	gln	val	tyr	gly	phe	val	arg	
CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	CGG	
470														480	
ala	cys	leu	arg	arg	leu	val	pro	pro	gly	leu	trp	gly	ser	arg	
GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	
490															
his	asn	glu	arg	arg	phe	leu	arg	asn	thr	lys	lys	phe	ile	ser	
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	
500														510	
leu	gly	lys	his	ala	lys	leu	ser	leu	gln	glu	leu	thr	trp	lys	
CTG	GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	
520															
met	ser	val	arg	asp	cys	ala	trp	leu	arg	arg	ser	pro	gly	val	
ATG	AGC	GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	
530														540	
gly	cys	val	pro	ala	ala	glu	his	arg	leu	arg	glu	glu	ile	leu	
GGC	TGT	GTT	CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	
550															
ala	lys	phe	leu	his	trp	leu	met	ser	val	tyr	val	val	glu	leu	
GCC	AAG	TTC	CTG	CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	
560														570	
leu	arg	ser	phe	phe	tyr	val	thr	glu	thr	thr	phe	gln	lys	asn	
CTC	AGG	TCT	TTC	TTT	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	
580															
arg	leu	phe	phe	tyr	arg	pro	ser	val	trp	ser	lys	leu	gln	ser	
AGG	CTC	TTT	TTC	TAC	CGG	CCG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	
590														600	
ile	gly	ile	arg	gln	his	leu	lys	arg	val	gln	leu	arg	glu	leu	
ATT	GGA	ATC	AGA	CAG	CAC	TTG	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	



FIGURE 53 (cont.)

610  
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630  
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
 pro ile val asn met asp tyr val val gly ala arg thr phe arg  
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660  
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670  
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690  
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700  
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720  
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730  
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750  
 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760  
 his gly his val arg lys ala phe lys ser his val ser thr leu  
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

FIGURE 53 (cont.)

770 780  
 thr asp leu gln pro tyr met arg gln phe val ala his leu gln  
 ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG  
 790  
 glu thr ser pro leu arg asp ala val val ile glu gln ser ser  
 GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC  
 800 810  
 ser leu asn glu ala ser ser gly leu phe asp val phe leu arg  
 TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CCC  
 820  
 phe met cys his his ala val arg ile arg gly lys ser tyr val  
 TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC  
 830 840  
 gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu  
 CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC  
 850  
 cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly  
 TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG  
 860 870  
 ile arg arg asp gly leu leu leu arg leu val asp asp phe leu  
 ATT CCG CCG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG  
 880  
 leu val thr pro his leu thr his ala lys thr phe leu arg thr  
 TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC  
 890 900  
 leu val arg gly val pro glu tyr gly cys val val asn leu arg  
 CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG  
 910  
 lys thr val val asn phe pro val glu asp glu ala leu gly gly  
 AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC  
 920 930  
 thr ala phe val gln met pro ala his gly leu phe pro trp cys  
 ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

FIGURE 53 (cont.)

940  
 gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr  
 GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950 960  
 ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn  
 TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970  
 arg gly phe lys ala gly arg asn met arg arg lys leu phe gly  
 CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980 990  
 val leu arg leu lys cys his ser leu phe leu asp leu gln val  
 GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000  
 asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu  
 AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010 1020  
 leu gln ala tyr arg phe his ala cys val leu gln leu pro phe  
 CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030  
 his gln gln val trp lys asn pro thr phe phe leu arg val ile  
 CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CCC GTC ATC

1040 1050  
 ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn  
 TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060  
 ala gly met ser leu gly ala lys gly ala ala gly pro leu pro  
 GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

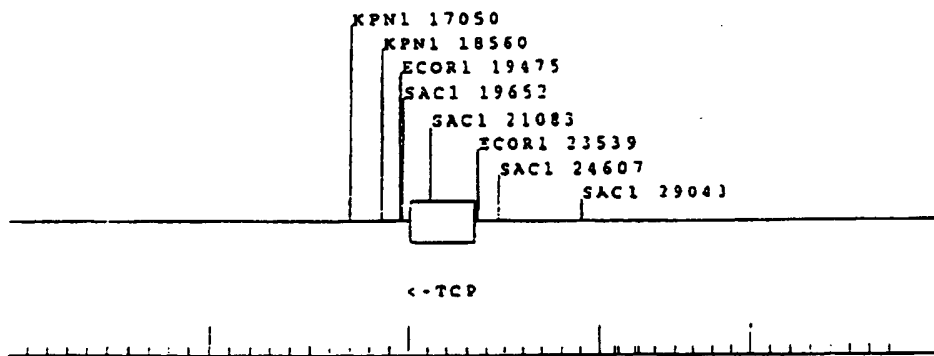
1070 1080  
 ser glu ala val gln trp leu cys his gln ala phe leu leu lys  
 TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090  
 leu thr arg his arg val thr tyr val pro leu leu gly ser leu  
 CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIGURE 53 (cont.)

1100 1110  
 arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr  
 AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG  
 1120  
 leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp  
 CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC  
 1130 1132  
 phe lys thr ile leu asp OP  
 TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA  
 CACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGCGGCCACACCC  
 AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC  
 GCCTGAAGGCTGAGTGTCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC  
 CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG  
 CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT  
 CGCCATTGTTACCCCYTCGCCCTGCCYTCTTTGCCTTCCACCCCCACCATCCAGGTGGA  
 GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA  
 CACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGTCAAAATGGGGGGAGGTGC  
 TGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAA

FIGURE 54



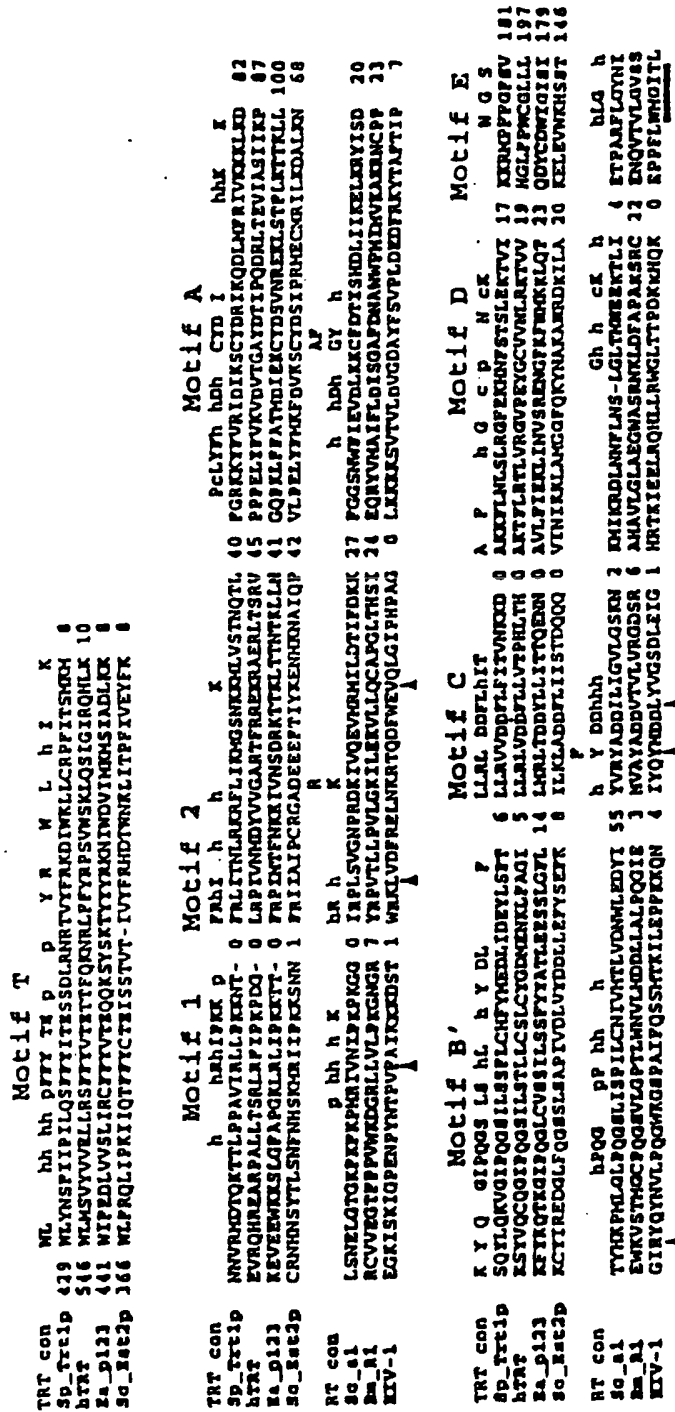


FIG. 55

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## mTART vs hTART align.adj Formatted Alignment

hTCP1.2.aa.gw	VVVVELLRSE FYVTETTFQK NRLFYTKGSV WSKLOSIGIR QHLKRVQLRE	600
mTART.1.aa.adj.gw	-----	
Consensus	.....	600
hTCP1.2.aa.gw	LSSEAVFQER EARHALL-LSARELRMRGOG IRETVNMDV VSRRTFFRER	649
mTART.1.aa.adj.gw	-----	43
Consensus	.....	650
hTCP1.2.aa.gw	FA-----SWVPPPS-IRNRRARRPGL LGASVLGLDHRRAWRTF	695
mTART.1.aa.adj.gw	-----	69
Consensus	.....	700
hTCP1.2.aa.gw	KVNRDOPPPF LYFVKVDVTG AYDTIPQDRL TEVLASIIKP QNTYCVRYA	745
mTART.1.aa.adj.gw	-----	79
Consensus	.....	750
hTCP1.2.aa.gw	VVQKAHGHV RKAFKSHVST LTDLQPYMRQ FVAHLQETSP LRDAVVTEQS	795
mTART.1.aa.adj.gw	-----	79
Consensus	.....	800
hTCP1.2.aa.gw	SSLNEASSGL FVVFLRFMCH HAVRIRGKSY VCCQGIPOGS ILSTLLCSLC	845
mTART.1.aa.adj.gw	-----	79
Consensus	.....	850
hTCP1.2.aa.gw	YGMENGLFA GINRGLLR LVDDPLLVTP NLTNARITLR TLVRGVPEYG	895
mTART.1.aa.adj.gw	-----	79
Consensus	.....	900
hTCP1.2.aa.gw	CVVNLKNTVV NPFVEDEALG GTAFVQMPAH GLFPWCGLLL DTRILEVQSD	945
mTART.1.aa.adj.gw	-----	79
Consensus	.....	950
hTCP1.2.aa.gw	YSSYARTSIR ASLTNRGFK AGRNRRKLF GVLRLKCHSL FLDLQVNSLQ	995
mTART.1.aa.adj.gw	-----	79
Consensus	.....	1000
hTCP1.2.aa.gw	TUCNIIYKIL LLQAVPSHAC VLQLDPMQGV WSRPTFFLRV ISDTASLCYS	1045
mTART.1.aa.adj.gw	-----	79
Consensus	.....	1050
hTCP1.2.aa.gw	ILKAGGAGMS LGAKGAGPL PSEAVQWLCH QAFLLKLTRH RVTYVPLIGS	1095
mTART.1.aa.adj.gw	-----	79
Consensus	.....	1100

FIG. 56 (1/2)

## mTRT.adj vs hTRT DNA align Formatted Alignment

hTCP1.2.gw	AGAGCACCGT CTGCOTGAGG AGATCCTGGC CAACTTCCTG CACTGCGTGA	1700
mTRT.1.adj.gw	-----	
Consensus	AGAGCACCGT CTGCOTGAGG AGATCCTGGC CAACTTCCTG CACTGCGTGA	1700
hTCP1.2.gw	TGAGTGTGTA CGTCOTGAGG CTGCTCAGGT CTTTCCTTTA TGTACGGAG	1750
mTRT.1.adj.gw	-----	
Consensus	TGAGTGTGTA CGTCOTGAGG CTGCTCAGGT CTTTCCTTTA TGTACGGAG	1750
hTCP1.2.gw	ACCACGTTTC AAAAGAACAG GCTCTTTTTC TACCGGAAGA GTGCTCGGAG	1800
mTRT.1.adj.gw	-----	
Consensus	ACCACGTTTC AAAAGAACAG GCTCTTTTTC TACCGGAAGA GTGCTCGGAG	1800
hTCP1.2.gw	CAAGTTGCA AGCATTGGAA TCAGACAGCA CTGGAAGAGG GTCCAGCTGC	1850
mTRT.1.adj.gw	-----	
Consensus	CAAGTTGCA AGCATTGGAA TCAGACAGCA CTGGAAGAGG GTCCAGCTGC	1850
hTCP1.2.gw	GGGAGCTGTC GGAAGCAGAG GTGCTGAGGAGG CAGGCTGAGG	1897
mTRT.1.adj.gw	-----	28
Consensus	GGGAGCTGTC GGAAGCAGAG GTGCTGAGGAGG CAGGCTGAGG	1900
hTCP1.2.gw	GGGAGCTGTC GGAAGCAGAG GTGCTGAGGAGG CAGGCTGAGG	1947
mTRT.1.adj.gw	-----	75
Consensus	GGGAGCTGTC GGAAGCAGAG GTGCTGAGGAGG CAGGCTGAGG	1950
hTCP1.2.gw	GGGAGCTGTC GGAAGCAGAG GTGCTGAGGAGG CAGGCTGAGG	1997
mTRT.1.adj.gw	-----	125
Consensus	GGGAGCTGTC GGAAGCAGAG GTGCTGAGGAGG CAGGCTGAGG	2000
hTCP1.2.gw	AAAGGAGC ----- CAGGCTGAGG CAGGCTGAGG	2035
mTRT.1.adj.gw	-----	163
Consensus	AAAGGAGC ----- CAGGCTGAGG CAGGCTGAGG	2050
hTCP1.2.gw	AAAGGAGC ----- CAGGCTGAGG CAGGCTGAGG	2085
mTRT.1.adj.gw	-----	205
Consensus	AAAGGAGC ----- CAGGCTGAGG CAGGCTGAGG	2100
hTCP1.2.gw	CTGGGCTTGG AGGCTGAGG CAGGCTGAGG CAGGCTTTC	2135
mTRT.1.adj.gw	-----	217
Consensus	CTGGGCTTGG AGGCTGAGG CAGGCTGAGG CAGGCTTTC	2150
hTCP1.2.gw	TGCTGCGTGT GCGCTGAGG CAGGCTGAGG CAGGCTTTC	2185
mTRT.1.adj.gw	-----	239
Consensus	TGCTGCGTGT GCGCTGAGG CAGGCTGAGG CAGGCTTTC	2200

FIG. 56 (2/2)

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## Telomerase Specific Motifs

Motif	MOTIF T	MOTIF T'
TRT con	W1	E V
hTRT	546 WLMSVVVELLRFFVYTETTFQKNRLEFYRKSVWSKLQSIGI	13 EAEVR
spTRT	429 WLYNSFIPIQLQSFYITESSDLRNRRTVYFRKDIWKLLCRPFI	12 ENNV
eaTRT	441 WIFEDLVVSLIRCFYVTEQQKSYSKTYYYRKNINWDVIMKMSI	12 EKEVE
scTRT	366 WLFRQLIPKIIQTFYCYCTEISSVT.IVYFRHDTWNKLIPTFI	9 ENNV

FIG. 57A

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# Telomerase RT Motifs (Fingers)

Motif	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R ipkk	fr I	p lyf D cyd I	Y q GIPQGs lS L Y
hTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI	104 YVQCQGIPOGSILSTLLCSLCY	
spTRT	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI	99 YLQKVGIPOGSILSSFLCHFYM	
aTRT	10 GKRLRIPKKTT 0 FRPIM	67 PKLFFATMDIEKCYDSV	117 YKQTKGIPOGGLCVSSILSSFY	
scTRT	13 SKMRIIPKKSN 2 FRIIA	68 PELYFMKFDVKSCYDSI	85 YIREDGLFQGSLSAPIVDLVY	
RT con	p hh h K	hr h	h hdh AF h	hpQG pp hh h
				GY

FIG. 57B

891107

# Telomerase RT Motifs (Palm, Primer Grip)

Motif	MOTIF C	MOTIF D	MOTIF E
TRT con	11111 Ddfl it	g n K	w g s 1
hTRT	15 LLLRLVDDFLVLT	15 GVPEYGCVVNLRKTVV	24 WCGLLLDTRTL
SPTRT	16 VLLRVVDDFLFIT	15 GFEKHNFSLEKTVI	22 FFGFSVNMRS
ATRT	24 LLMRLTDDYLLIT	15 VSRENGFKFNKKLQT	28 WIGISIDMKTL
SCRTT	18 LILKLADDFLIIS	15 GFQKYNANRDKILA	25 WKHSSTMNNFH
RT con	h y DDhhh F	Gh h cK h	hLG h

FIG. 57C

for 109

FIGURE 58

```

1
met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

40
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

50
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

60
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

70
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

80
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

90
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GCG AGC GGG GCG

```

			140											150		
trp	gly	leu	leu	leu	arg	arg	val	gly	asp	asp	val	leu	val	his		
TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	GAC	GAC	GTG	CTG	GTT	CAC		
								160								
leu	leu	ala	arg	cys	ala	leu	phe	val	leu	val	ala	pro	ser	cys		
CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	GTG	GCT	CCC	AGC	TGC		
			170											180		
ala	tyr	gln	val	cys	gly	pro	pro	leu	tyr	gln	leu	gly	ala	ala		
GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	CTC	GGC	GCT	GCC		
								190								
thr	gln	ala	arg	pro	pro	pro	his	ala	ser	gly	pro	arg	arg	arg		
ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	CGA	AGG	CGT		
			200											210		
leu	gly	cys	glu	arg	ala	trp	asn	his	ser	val	arg	glu	ala	gly		
CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	GCC	GGG		
								220								
val	pro	leu	gly	leu	pro	ala	pro	gly	ala	arg	arg	arg	gly	gly		
GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	CCG	AGG	AGG	CGC	CGG	GGC		
			230											240		
ser	ala	ser	arg	ser	leu	pro	leu	pro	lys	arg	pro	arg	arg	gly		
AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC		
								250								
ala	ala	pro	glu	pro	glu	arg	thr	pro	val	gly	gln	gly	ser	trp		
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG		
			260											270		
ala	his	pro	gly	arg	thr	arg	gly	pro	ser	asp	arg	gly	phe	cys		
GCC	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT		
								280								
val	val	ser	pro	ala	arg	pro	ala	glu	glu	ala	thr	ser	leu	glu		
GTG	GTG	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG		

**FIGURE 58 (cont.)**

290														300		
gly	ala	leu	ser	gly	thr	arg	his	ser	his	pro	ser	val	gly	arg		
GGT	GCG	CTC	TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA	TCC	GTG	GGC	CGC		
310																
gln	his	his	ala	gly	pro	pro	ser	thr	ser	arg	pro	pro	arg	pro		
CAG	CAC	CAC	GCG	GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA	CCA	CGT	CCC		
320														330		
trp	asp	thr	pro	cys	pro	pro	val	tyr	ala	glu	thr	lys	his	phe		
TGG	GAC	ACG	CCT	TGT	CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG	CAC	TTC		
340																
leu	tyr	ser	ser	gly	asp	lys	glu	gln	leu	arg	pro	ser	phe	leu		
CTC	TAC	TCC	TCA	GGC	GAC	AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC	CTA		
350														360		
leu	ser	ser	leu	arg	pro	ser	leu	thr	gly	ala	arg	arg	leu	val		
CTC	AGC	TCT	CTG	AGG	CCC	AGC	CTG	ACT	GGC	GCT	CGG	AGG	CTC	GTG		
370																
glu	thr	ile	phe	leu	gly	ser	arg	pro	trp	met	pro	gly	thr	pro		
GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	CCC	TGG	ATG	CCA	GGG	ACT	CCC		
380														390		
arg	arg	leu	pro	arg	leu	pro	gln	arg	tyr	trp	gln	met	arg	pro		
CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	TAC	TGG	CAA	ATG	CGG	CCC		
400																
leu	phe	leu	glu	leu	leu	gly	asn	his	ala	gln	cys	pro	tyr	gly		
CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	CAG	TGC	CCC	TAC	GGG		
410														420		
val	leu	leu	lys	thr	his	cys	pro	leu	arg	ala	ala	val	thr	pro		
GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	GCG	GTC	ACC	CCA		
430																
ala	ala	gly	val	cys	ala	arg	glu	lys	pro	gln	gly	ser	val	ala		
GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	TCT	GTG	GCG		

FIGURE 5B (cont.)

440 450  
 ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
 GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460  
 leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
 CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480  
 ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
 GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490  
 his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
 CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510  
 leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
 CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACC TGG AAG

520  
 met ser val arg asp cys ala trp leu arg arg ser pro gly val  
 ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540  
 gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
 GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550  
 ala lys phe leu his trp leu met ser val tyr val val glu leu  
 GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570  
 leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
 CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580  
 arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser  
 AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

590 600  
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

## FIGURE 58 (cont.)

610  
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630  
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
 pro ile val asn met asp tyr val val gly ala arg thr phe arg  
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660  
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670  
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690  
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700  
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720  
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730  
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750  
 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760  
 his gly his val arg lys ala phe lys ser his val ser thr leu  
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG



## FIGURE 5B (cont.)

```

              770                                780
thr asp leu gln pro tyr met arg gln phe val ala his leu gln
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

              790
glu thr ser pro leu arg asp ala val val ile glu gln ser ser
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

              800                                810
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

              820
phe met cys his his ala val arg ile arg gly lys ser tyr val
TTC ATG TGC CAC CAC GCC CTG CGC ATC AGG GGC AAG TCC TAC GTC

              830                                840
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

              850
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTC TTT GCG GGC

              860                                870
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
ATT CCG CCG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

              880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

              890                                900
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

              910
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

              920                                930
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

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FIGURE 58 (cont.)

940  
 gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr  
 GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950 960  
 ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn  
 TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970  
 arg gly phe lys ala gly arg asn met arg arg lys leu phe gly  
 CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980 990  
 val leu arg leu lys cys his ser leu phe leu asp leu gln val  
 GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000  
 asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu  
 AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010 1020  
 leu gln ala tyr arg phe his ala cys val leu gln leu pro phe  
 CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030  
 his gln gln val trp lys asn pro thr phe phe leu arg val ile  
 CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040 1050  
 ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn  
 TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060  
 ala gly met ser leu gly ala lys gly ala ala gly pro leu pro  
 GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070 1080  
 ser glu ala val gln trp leu cys his gln ala phe leu leu lys  
 TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090  
 leu thr arg his arg val thr tyr val pro leu leu gly ser leu  
 CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

## FIGURE 5b (cont.)

```

                                1100                                1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

                                1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

                                1130      1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCACACCC
AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC
GGCTGAAGGCTGAGTGTCGGGCTGAGGCCTGAGCGAGTGTCAGCCAAAGGCTGAGTGTC
CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
CGCCATTGTTACCCYTCGCCCTGCCYTCTTTGCCTTCCACCCCCACCATCCAGGTGGA
GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
CACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATGGGGGGAGGTGC
TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAA
AAAAAAAAAA

```

## FIGURE 59

(page 1 of 7 for Fig. 59: SEQ ID NO:122/123)

1  
met  
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG  
ATG

10  
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20 30  
his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40  
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50 60  
phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70  
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80 90  
leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100  
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110 120  
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

130  
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

SEQ ID NO:122/123: (page 2 of 7 for Fig. 59: SEQ ID NO:122/123)

140 150  
trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

160  
leu leu ala arg cys ala leu phe val leu val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170 180  
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

190  
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

200 210  
leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220  
val pro leu gly leu pro ala pro gly ala arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230 240  
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

250  
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260 270  
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

280  
val val ser pro ala arg pro ala glu glu ala thr ser leu glu  
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

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SEQ ID NO:122/123: (page 3 of 7 for Fig. 59: SEQ ID NO:122/123)

290 300  
gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310  
gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330  
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340  
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360  
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370  
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390  
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400  
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420  
val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430  
ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

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SEQ ID NO:122/123: (page 4 of 7 for Fig. 59: SEQ ID NO:122/123)

440 450  
ala pro glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460  
leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480  
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490  
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510  
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520  
met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540  
gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550  
ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570  
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580  
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

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SEQ ID NO:122/123: (page 5 of 7 for Fig. 59: SEQ ID NO:122/123)

590 600  
ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610  
ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630  
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660  
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670  
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690  
gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700  
thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720  
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730  
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

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SEQ ID NO:122/123: (page 6 of 7 for Fig. 59: SEQ ID NO:122/123)

740

750

asn thr tyr cys val arg arg tyr ala val val gln lys ala ala

AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760

his gly his val arg lys ala phe lys ser his val leu arg pro

CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770

780

val pro gly asp pro ala gly leu his pro leu his ala ala leu

GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

790

gln pro val leu arg arg his gly glu gln ala val cys gly asp

CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

800

807

ser ala gly arg ala ala pro ala phe gly gly OP

TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA

TTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGT  
CCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGC GGAAGACAGTGGTGAACCT  
CCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTTCAGATGCCGGCCACGG  
CCTATTCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGA  
CTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTT  
CAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTC  
ACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT  
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCAT  
TTCATCAGCAAGTTTGGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGG  
CCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCA  
AGGGCGCCGCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCA  
TTCCTGCTCAAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTC  
AGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCT  
GGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGAT  
GGCCACCCGCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTCACGCCGGG  
CTCTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGT  
CTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGT  
CCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCCAGCACACCTGCC  
GTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCAGGGCCAGCTTTTCTCTCA

SEQ ID NO:122/123: (page 7 of 7 for Fig. 59: SEQ ID NO:122/123)

CCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATT  
GTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCC  
TGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTAC  
ACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGGAGG  
TGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

Translated Mol. Weight = 90239.69

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**FIGURE 60**  
**MOUSE TRT SEQUENCE**

(SEQ ID NO:124; page 1 of 2)

```
1   CGGGTGGGAGGCCCATCCCGGCCTTGAGCACAATGACCCGCGCTCCTCGT
51  TGCCCCGCGGTGCGCTCTCTGCTGCGCAGCCGATACCGGGAGGTGTGGCC
101 GCTGGCAACCTTTGTGCGGCGCCTGGGGCCCCGAGGGCAGGCGGCTTGTGC
151 AACCCGGGGACCCGAAGATCTACCGCACTTTGGTTGCCAATGCCTAGTG
201 TGCATGCACTGGGGCTCACAGCCTCCACCTGCCGACCTTTCCTTCCACCA
251 GGTGTCATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGCAGAGACTCTGCG
301 AGCGCAACGAGAGAAACGTGCTGGCTTTTGGCTTTGAGCTGCTTAACGAG
351 GCCAGAGGCGGGCCTCCCATGGCCTTCACTAGTAGCGTGCCTAGCTACTT
401 GCCCAACACTGTTATTGAGACCCTGCGTGTCAAGTGGTGCATGGATGCTAC
451 TGTTGAGCCGAGTGGGCGACGACCTGCTGGTCTACCTGCTGGCACACTGT
501 GCTCTTTATCTTCTGGTGCCCCCAGCTGTGCCTACCAGGTGTGTGGGTC
551 TCCCCTGTACCAAATTTGTGCCACCACGGATATCTGGCCCTCTGTGTCCG
601 CTAGTTACAGGCCCCACCCGACCCGTGGGCAGGAATTTCACTAACCTTAGG
651 TTCTTACAACAGATCAAGAGCAGTAGTCGCCAGGAAGCACCGAAACCCCT
701 GGCCTTGCCATCTCGAGGTACAAAGAGGCATCTGAGTCTCACCAGTACAA
751 GTGTGCCTTCAGCTAAGAAGGCCAGATGCTATCCTGTCCCGAGAGTGGAG
801 GAGGGACCCACAGGCAGGTGCTACCAACCCCATCAGGCAAATCATGGGT
851 GCCAAGTCCTGCTCGGTCCCCCGAGGTGCCTACTGCAGAGAAAGATTTGT
901 CTTCTAAAGGAAAGGTGTCTGACCTGAGTCTCTCTGGGTGCGGTGTGCTGT
951 AAACACAAGCCCAGCTCCACATCTCTGCTGTCAACACCCCGCCAAAATGC
1001 CTTTCAGCTCAGGCCATTTATTGAGACCAGACATTTCTTTACTCCAGGG
1051 GAGATGGCCAAGAGCGTCTAAACCCCTCATTCTACTCAGCAACCTCCAG
1101 CCTAACTTGACTGGGGCCAGGAGACTGGTGGAGATCATCTTTCTGGGCTC
1151 AAGGCCTAGGACATCAGGACCACTCTGCAGGACACACCGTCTATCGCGTC
1201 GATACTGGCAGATGCGGCCCTGTTCCAACAGCTGCTGGTGAACCATGCA
1251 GAGTGCCAATATGTCAGACTCCTCAGGTCACATTGCAGGTTTCGAACAGC
1301 AAACCAACAGGTGACAGATGCCTTGAACACCAGCCCACCGCACCTCATGG
1351 ATTTGCTCCGCCTGCACAGCAGTCCCTGGCAGGTATATGGTTTTCTTCGG
1401 GCCTGTCTCTGCAAGGTGGTGTCTGCTAGTCTCTGGGGTACCAGGCACAA
1451 TGAGCGCCGCTTCTTTAAGAACTTAAAGAAGTTCATCTCGTTGGGGAAAT
1501 ACGGCAAGCTATCACTGCAGGAACTGATGTGGAAGATGAAAGTAGAGGAT
1551 TGCCACTGGCTCCGCAGCAGCCCGGGGAAGGACCGTGTCCCGCTGCAGA
1601 GCACCGTCTGAGGGAGAGGATCCTGGCTACGTTCTCTGTTCTGGCTGATGG
1651 ACACATACGTGGTACAGCTGCTTAGGTCATTCTTTTACATCACAGAGAGC
1701 ACATTCCAGAAGAACAGGCTCTTCTTCTACCGTAAGAGTGTGTGGAGCAA
1751 GCTGCAGAGCATTGGAGTCAGGCAACACCTTGAGAGAGTGCGGCTACGGG
1801 AGCTGTCACAAGAGGAGGTCAGGCATCACCAGGACACCTGGCTAGCCATG
1851 CCCATCTGCAGACTGCGCTTCATCCCCAAGCCCAACGGCCTGCGGCCCAT
1901 TGTGAACATGAGTTATAGCATGGGTACCAGAGCTTTGGGCAGAAAGGAAGC
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(figure 60, SEQ ID NO:124; page 2 of 2)

```
1951 AGGCCCAGCATTTCACCCAGCGTCTCAAGACTCTCTTCAGCATGCTCAAC
2001 TATGAGCCGACAAAACATCCTCACCTTATGGGGTCTTCTGTACTGGGTAT
2051 GAATGACATCTACAGGACCTGGCGGGCCTTTGTGCTGCGTGTGCGTGCTC
2101 TGGACCANACACCANGATGTACTTTGTTAAGGCAGATGTGACCGGGGCCT
2151 ATGATGCCATCCCCAGGGTAAGCTGGGTGNNNNNNNNNNNNNNNNNNNNNN
2201 NNNNNNNNNNNNNNNNNNNNNNNNTGGTGGAGGTTGTTGCCAATATGATCAGGC
2251 ATTCGGAGAGCACGTACTGTATCCGCCAGTATGCAGTGGTCCGGAGAGAT
2301 AGCCAAGGCCAAGTCCACAAGTCNTTTAGGAGACAGGTCACCACCTTCTC
2351 TGACTTCCAGCCATACATGGGCCAGTTCCTTAAGCATCTGCAGGATTGAG
2401 ATGCCAGTGCACTGAGGAACTCCGTTGTCATCGAGCAGAGCATCTCTATG
2451 AATGAGAGCAGCAGCAGCCTGTTTGATTCTTCCTGCACTTCCTGCGTCAC
2501 AGTGTCGTAAAGATTGGTGACAGGTGCTATACGCAGTGCCAGGGCATCCC
2551 CCAGGGCTCCAGCCTATCCACCCTGCTCTGCAGTCTGTGTTTCGGAGACA
2601 TGGAGAACAAGCTGTTTGCTGAGGTGCAGCGGGATGGGTGCTTTTACGT
2651 TTTGTTGATGACTTTCTGTTGGTGACGCCTCACTTGGACCAAGCAXXXX
2701 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2751 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2801 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2851 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCTGCAGTTAT
2901 GCCCAGACCTCAATTAAGACGAGCCTCACCTTCCAGAGTGTCTTCAAAGC
2951 TGGGAAGACCATGCGGAACAAGCTCCTGTCTGGTCTTGCGGTTGAAGTGTC
3001 ACGGTCTATTTCTAGACTTGCAGGT
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